Relationships Between Average Income Per Person and County's Economic, Health and Social Well-being

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Abstract

We address the question of how average income per person was related to other variables associated with the county's economic, health and social well-being. We examine data on the county demographic information (CDI) for 440 of the most populous counties in the United States selected by Kutner et al. (2005). From our analysis, it appears the correlations came in a group of five and were all strongly correlated with each other, which consist of crimes, population, total income, doctors and hospital beds. Besides, the percent of population that have high school degree are highly correlated with the percent of population that are below poverty level, and the percent of population aged 18–34 is also highly negatively correlated with the percent of population aged 65 or older. More job opportunities, more well-paid jobs, higher education and better social well-being are essential for increasing average per-capita income in a county. Also there does existed a relationship between income per person and the geographic features and the composition of population of the county, including region and land area. Since our data and analysis only cover 373 counties, the study in this paper was also limited by the size of the data set.

1 Introduction

Per-capita income has always been a topic of high concern among economists, statisticians and ordinary people, which may be influenced many factors. How will average income per person be related with economic, health and social well-being?

In this paper, we have been asked to explore the relationships between average per-capita income and county's economic, health, social Well-being, and predict it from all the influence factors. Relationships may vary depending on the geographical scope of the study, and the emphasis may also vary. Particularly, we are focusing on the counties.

In addition to answering the main question posed above, we will address the following questions:

- Is there any relationships between all the influence factors? If so, how they effect each other?
- Is there a relationship between per-capita income and crime rate? And how does this relationship differentiate in different regions of the country?
- Is there a best model predicting per-capita income from the other variables? If so, what is that?
- Since we only cover 373 of approximately 3000 counties in the US, will the accuracy of the study affected by the missing counties? Why or why not?

2 Data

The data for this study is taken from Kutner et al. (2005). It provides selected county demographic information (CDI) for 440 of the most populous counties in the United States, and the information generally pertains to the years 1990 and 1992. The reader should refer to Kutner et al. (2005) for definitions, eligibility, inclusion/exclusion criteria, and so forth. See the relationships between all variables in Figure 1.

Variable Number	Variable Name	Description
1	Identification number	1–440
2	County	County name
3	State	Two-letter state abbreviation
4	Land area	Land area (square miles)
5	Total population	Estimated 1990 population
6	Percent of population aged 18–34	Percent of 1990 CDI population aged 18–34
7	Percent of population 65 or older	Percent of 1990 CDI population aged 65 or old
8	Number of active physicians	Number of professionally active non federal physicians during 1990
9	Number of hospital beds	Total number of beds, cribs, and bassinets during 1990
10	Total serious crimes	Total number of serious crimes in 1990, including murder, rape, robbery, aggravated assault, burglary, larceny-theft, and motor vehicle theft, as reported by law enforcement agencies
11	Percent high school graduates	Percent of adult population (persons 25 years old or older) who completed 12 or more years of school
12	Percent bachelor's degrees	Percent of adult population (persons 25 years old or older) with bachelor's degree
13	Percent below poverty level	Percent of 1990 CDI population with income below poverty level
14	Percent unemployment	Percent of 1990 CDI population that is unemployed
15	Per capita income	Per-capita income (i.e. average income per person) of 1990 CDI population (in dollars)
16	Total personal income	Total personal income of 1990 CDI population (in millions of dollars)
17	Geographic region	Geographic region classification used by the US Bureau of the Census, NE (northeast region of the US), NC (north-central region of the US), S (southern region of the US), and W (Western region of the US)

Table 1: Definitions of All variables.

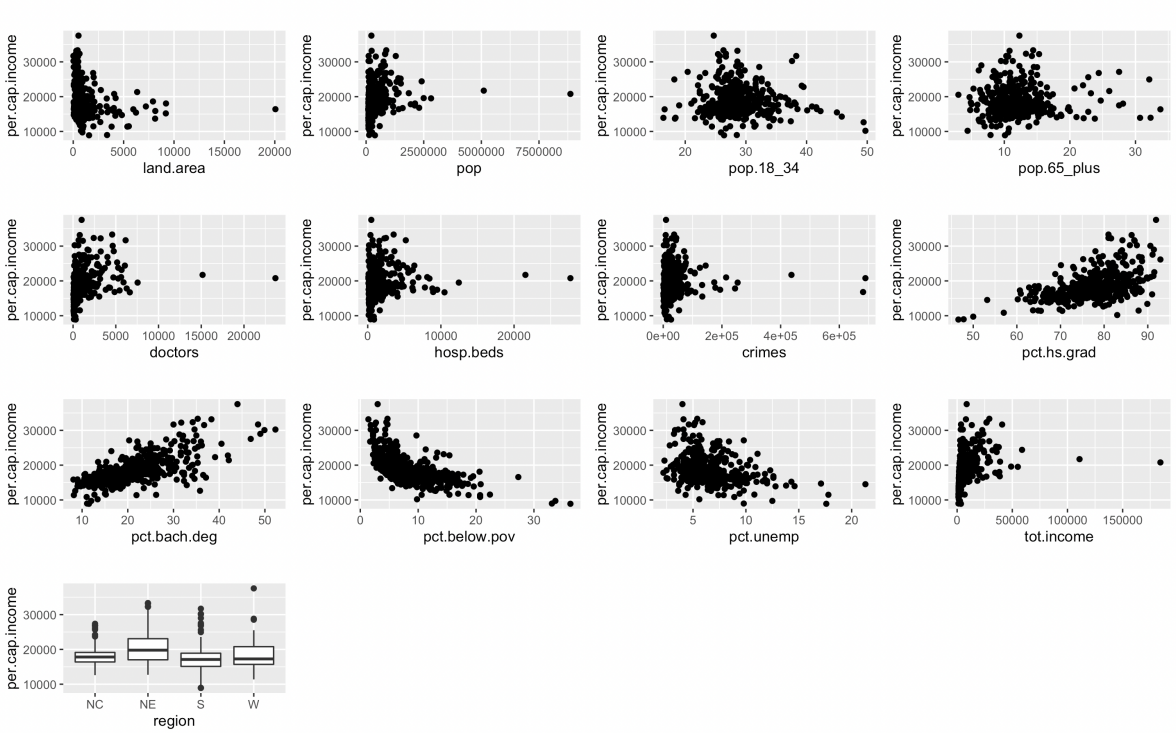

Figure 1: Scatterplot matrix of CDI(county demographic information).

In all, 440 of the most populous counties' CDI in the United States are represented in the data available to us, and the variables were defined in the following Table 1:

In Figure 1 we show the relationships between all of the quantitative variables in the data. Some of them appear to be linearly correlated with the response variable per-capita income, and the distribution of some quantitative variables is highly skewed (Appendix 1), indicating transformation. Table 2 and Table 3 provide us with a quick summaries of the numeric variables and character variables we will be using in this paper.

3 Methods

First, we did the visual comparison of exploratory scatter plots and histograms to check univariable distributions, using the R language and environment for statistical computing (R Core Team, 2017). And in order to identify any relationships may exist between all the influence factors, we have also examined the raw data in cdi.dat using exploratory scatter plots (see Figure 1) and a correlation plot. We used logarithm transformation on some variables to overcome non-linearity and skewness of variable distribution. Detailed analysis can be found in Appendix 1.

Then, to address the question about whether per-capita income is related to crime rate, and how this relationship may be different in different regions of the country, we used three multiple regression models. This analysis can tell us about the existence of the relationship and the effect of region, after controlling for all the other predictor variables. After that, by replacing the number of crimes with per-capita crimes, we examined whether different scales of a variable affect its influence on predictor variable, and we compared two best models selected using AIC and BIC. Detailed R analyses can be found in Appendix 2 (pg.9).

Next, we considered multiple regression models, also in R, to fit the best model predicting per-capita income from all the other variables except population and total income, which are two deterministic factors for per-capita income. And we converted land area, doctors, hospital beds, crimes and total income into per-capita scales for better interpretation. For further model selection, we first chose a best model with all possible subsets method by comparing AIC, AICc and BIC; then, another best model was chosen from step-wise regression; lastly, based on LASSO regression and cross-validation

Numeric Variables				
Variables	Min.	Median	Mean	Max.
id	1.0	220.5	220.5	440.0
land.area	15.0	656.5	1041.4	20062.0
pop	100043	217280	393011	8863164
pop.18.34	16.40	28.10	28.57	49.70
pop.65.plus	3.000	11.750	12.170	33.800
doctors	39.0	401.0	988.0	23677.0
hosp.beds	92.0	755.0	1458.6	27700.0
pct.hs.grad	46.60	77.70	77.56	92.90
pct.bach.deg	8.10	19.70	21.08	52.30
pct.below.pov	1.400	7.900	8.721	36.300
pct.unemp	2.200	6.200	6.597	21.300
per.cap.income	8899	17759	18561	37541
tot.income	1141	3857	7869	184230

Table 2: Summary for Numeric Variables.

Character variables				
	NC	NE	S	W
Freq	108	103	152	77

Table 3: Summary for Character Variables.

using mean-squared prediction error, we had another best model.

We examined case-wise residual plots, marginal model plots, partial-regression and a likelihood ratio test to select the best model. That model is used to interpret the effects of the predictor variables and to estimate per-capita income with county's economic, health, social Well-being. This final model also tells us about the effect of each individual predictor variable, after controlling for all the other predictor variables. Details of these analyses in R can be found in Appendices 3, 4 and 5.

Finally, to answer the fourth question, no analysis was conducted and discussion points were made in the discussion section of this paper.

4 Results

4.1 Exploratory Plots and Transformation

First, from the histograms of the distribution of raw data (see the distribution plot in Appendix 1, pg.3) and Table 2, we found that land area, population, doctors, hospital beds, crimes ,total income need transformation, since they are severely right-skewed.

In the correlation matrix (See Figure 2), it suggests that we may run into multi-collinearity problems when we start fitting models. In Figure 2, the correlations came in a group of five and were all strongly positively correlated with each other, which consist of crimes, population, total income, doctors and hospital beds. Besides, the percent of population that have high school degree are highly negatively correlated with the percent of population that are below poverty level, and the percent of population aged 18–34 is also highly negatively correlated with the percent of population aged 65 or older. Other than that, three variables, including the percent of population have bachelor's degree, the percent of population that have high school degree and per-capita income, are moderately positively correlated with each other.

To address heavy skewing and potential leverage and influence issues, we only took the logarithms of the variables we identified earlier, and we also consider logarithms transformation for per-capita income. As we can see from Figure 3, the skewing seems to have largely been brought under control after transformation.

We also consider logarithms transformation for per ca-pita income. As we can see from Figure 3, the skewing seems to have largely been brought under control after transformation.

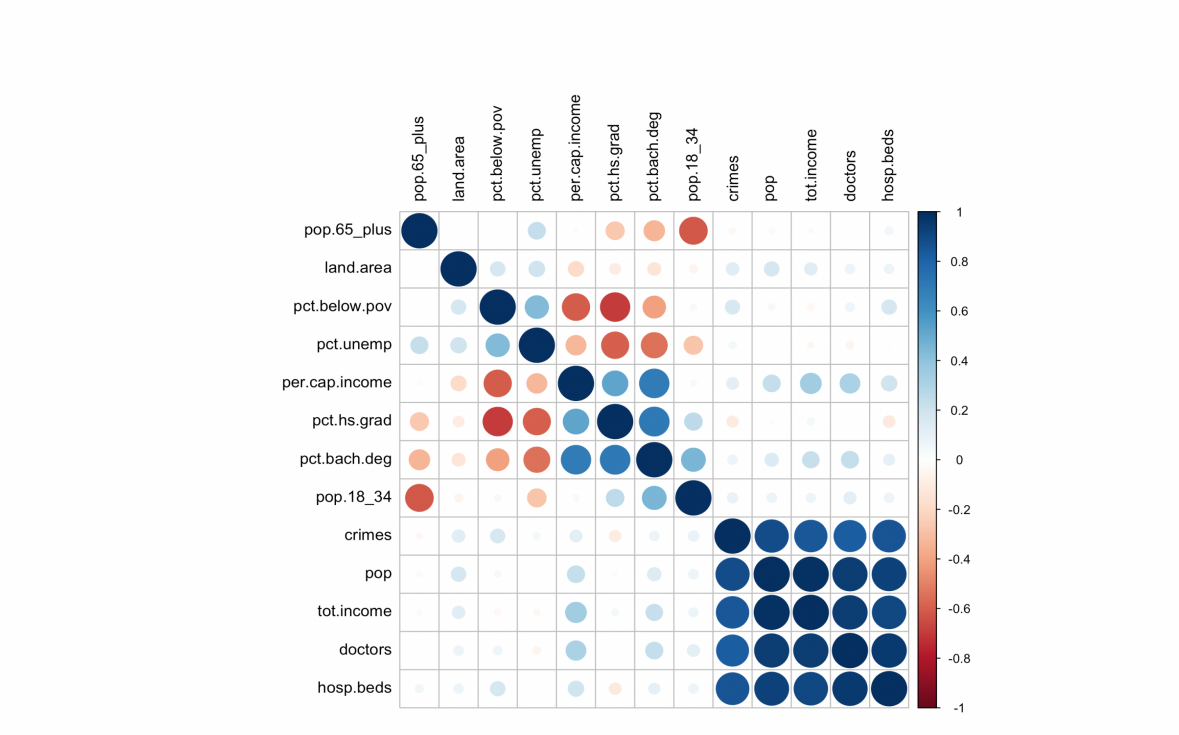

Figure 2: Correlation Matrix of CDI(county demographic information).

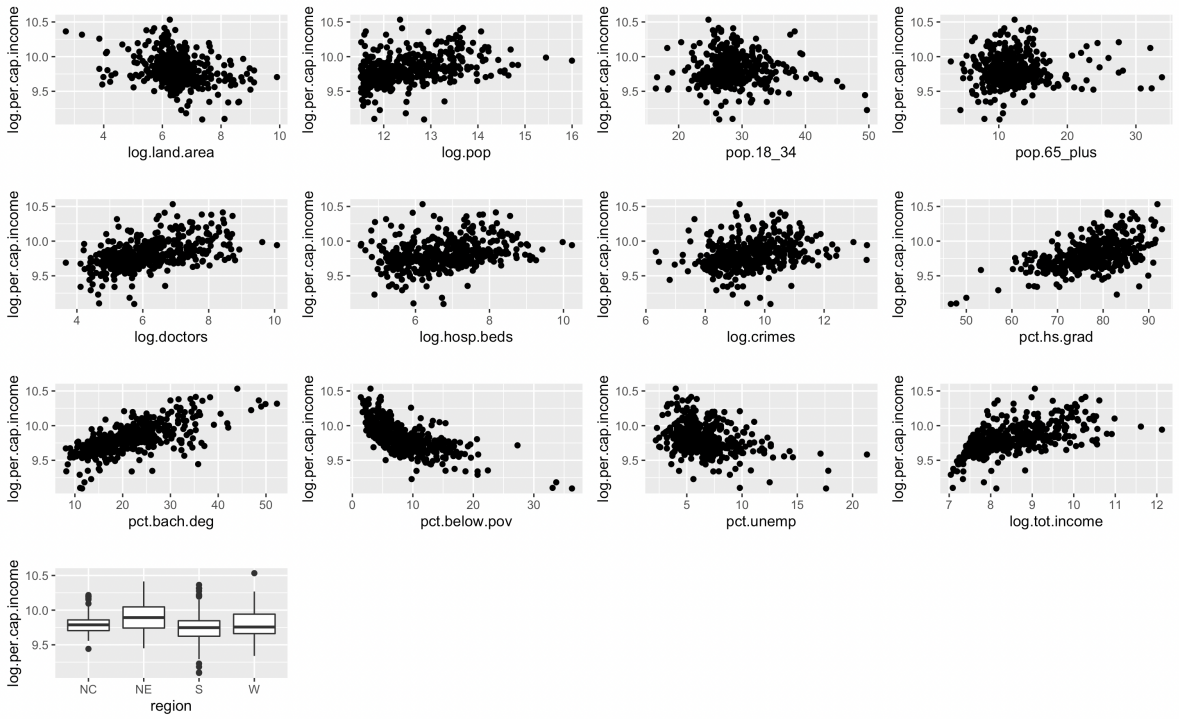

Figure 3: Scatterplot matrix of Transformed CDI(county demographic informations).

	Estimate	Std. Error	t value	$Pr(>\|t\|)$
β_0 :(Intercept)	9.94	0.07	143.30	0.00
β_1 :log(per.cap.crimes)	0.04	0.02	1.98	0.05
β_2 :regionNE	0.11	0.03	4.15	0.00
β_3 :regionS	-0.07	0.03	-2.84	0.00
β_3 :regionW	-0.02	0.03	-0.81	0.42

Table 4: Estimated coefficients for model(5).

4.2 Relationship between Per Capita Income and Crime Rate

Since logarithms cleaned up a lot of the skewing in the data, we will only use log-transformed variables from now on for regression. For the income and each version of crime variables, there are essentially three models to think about.

First, for log.per.cap.income and log.crimes, the three models to consider are:

$$\log(per.cap.income) = \beta_0 + \beta_1 * log(crimes) \tag{1}$$

$$\log(per.cap.income) = \beta_0 + \beta_1 * log(crimes) + \beta_2 * region \tag{2}$$

$$\log(per.cap.income) = \beta_0 + \beta_1 * log(crimes) + \beta_2 * region + \beta_3 * log(crimes) * region \tag{3}$$

In order to compare this with a model involving "per capita crime", we have to construct a new variable, and we will look at the same three models with this new variable.

$$\log(per.cap.income) = \beta_0 + \beta_1 * log(per.cap.crimes) \tag{4}$$

$$\log(per.cap.income) = \beta_0 + \beta_1 * log(per.cap.crimes) + \beta_2 * region \tag{5}$$

$$\log(per.cap.income) = \beta_0 + \beta_1 * log(per.cap.crimes) + \beta_2 * region + \beta_3 * log(per.cap.crimes) * region \tag{6}$$

We compared all 6 models with AIC or BIC, and from that, we get the result: the second model (named as "ancova.02" in Appendix 2) has both the lowest AIC and the lowest BIC values (Appendix 2, pg.9). However, there is an argument that per capita crime is more comparable to, or at least on the same scale as, per capita income. Thus, for better interpretation, we finally decide on the model (5).

Table 4 gives the estimated coefficients for model (5) along with standard errors and the usual t-test for testing whether each coefficient is significantly different from zero. All across the US, for every 1% increase in per capita crime, there is an associated 0.04% increase in per capita income. And the regional baseline salaries are: NC: \$20,743.74, NE: \$23,155.79, S: \$19,341.34, and W: \$20,332.99. All but the W region have baselines that are, according to the model, significantly different from the NC baseline. So, according to the model (5), the level of salary varies with region in the US, but the way it is related to crime does not.

4.3 Regression Analysis

Since there are 373 counties and 48 states in our data set, which means too many levels for a categorical variable. Thus, to make the analysis simpler, we will not consider the specific geographic identifiers like: "county" and "state", instead we will only use 4 different regions in "Geographic region" as 4 dummy variables for identifying. Per capita variables are more comparable to, or at least on the same scale as, per capita income, so we will convert land area, doctors, hospital beds, crimes and total income into per capita scales. And we took population and total income out of consideration for regression and per capita income is a deterministic function of them. And there are three methods we will be using for model selection, including all subsets, step-wise regression and LASSO.

First in all subsets regression, by locating the model with the lowest BIC, we found the best model 7 in all subsets regression.

$$\begin{aligned}\log(per.cap.incom) =&\beta_0 + \beta_1 * log(per.cap.land.area) + \beta_2 * pop.18\_34 \\ &+ \beta_3 * pop.65\_plus + \beta_4 * log(per.cap.doctors) \\ &+ \beta_5 * pct.hs.grad + \beta_6 * pct.bach.deg \\ &+ \beta_7 * pct.below.pov + \beta_8 * pct.unemp\end{aligned} \tag{7}$$

All the predictors have coefficients significantly different from zero. However, most of the coefficients are small, and some seem to have the wrong sign (e.g. *pct.hs.grad* and *pct.unemp*) (Appendix 3, pg.15).

Next, we added the interaction with region. Following the rule: when selecting categorical variables, if any indicator in a category seems important, then we will keep the whole category; or if none of them seem important, then we shall drop the categorical variable, we found another best model 8. After checking VIFs and diagnostics, and comparing to the best BIC model 7 that we obtained from subsets without the *region* term (Appendix 4, pg.23), we arrive at the final model 8 with interaction of region.

$$\begin{aligned}\log(per.cap.income) =&\beta_0 + \beta_1 * log(per.cap.land.area) + \beta_2 * pop.18\_34 \\ &+ \beta_3 * pop.65\_plus + \beta_4 * log(per.cap.doctors) \\ &+ \beta_5 * pct.hs.grad + \beta_6 * pct.bach.deg \\ &+ \beta_7 * pct.below.pov + \beta_8 * pct.unemp \\ &+ \beta_9 * region + \beta_{10} * (log(per.cap.land.area) : region) \\ &+ \beta_{11} * (log(per.cap.doctors) : region) + \beta_{12} * (pct.hs.grad : region) \\ &+ \beta_{13} * (pct.below.pov : region) + \beta_{14} * (pct.unemp : region)\end{aligned} \tag{8}$$

Table 5 gives the estimated coefficients for model (8) along with standard errors and the usual t-test for testing whether each coefficient is significantly different from zero.

As seen above, for every 1% increase in a county's per capita land area, there is a 0.05% decrease in expected per capita income. However, in South and West, a one percentage point increase in county's per capita land area induces an expected 0.01% and 0.03% increase in per capita income. For every 1% increase in per capita doctors in a county, the expected per capita income increases by about 0.05%. For all regions, increase in the number of per capita doctors induces increase in per capita average income, especially in West, where a one percentage point increase in per capita doctors induces an expected 0.12% increase in per capita income.

For every 1 percentage point increase in the percent of the population aged 18-34, there is an expected 2% drop in per capita income. However, percent of the population that are 65 years old and over doesn't have much effect on per capita income.

Percent of the population that are high school graduates doesn't have much effect, except in the West, where a one percentage point increase in high school graduates induces an expected 2% decrease in per capita income.

And for every 1% increase in percent of the population that have a bachelor's degree, there is a 1% increase in expected per capita income. For every 1% increase in percent of percent below poverty level, there is a 2% decrease in expected per capita income.

And in the main effect for region, and in several of the interactions for region, the West shows up as deviating significantly from the North Central part of the US.

Then, we used two stepwise regressions, including AIC and BIC. And in the stepwise regression using the BIC criterion, we actually found the model that is exactly the same as the all-subsets model 8 (Appendix 4, pg.23). We also explored 2-way interactions briefly, and both AIC and BIC like models with some interactions, as we can see in Table 6. However, the model is just getting too complicated to explain to someone.

In conclusion, we shall stick with the model found by all-subsets and stepAIC with a BIC penalty, and we will once again be led to model 8 we found based on the all-subsets, which is most interesting and interpretable.

	Estimate	Std. Error	t value	$Pr(>\|t\|)$
β_0 :(Intercept)	10.27	0.28	36.06	0.00
β_1 :log.per.cap.land.area	-0.05	0.01	-5.86	0.00
β_2 :pop.18_34	-0.02	0.00	-11.93	0.00
β_3 :pop.65_plus	0.00	0.00	-1.33	0.19
β_4 :log.per.cap.doctors	0.05	0.02	3.10	0.00
β_5 :pct.hs.grad	0.00	0.00	-1.14	0.25
β_6 :pct.bach.deg	0.01	0.00	15.14	0.00
β_7 :pct.below.pov	-0.02	0.00	-6.03	0.00
β_8 :pct.unemp	0.02	0.00	3.72	0.00
β_9 :regionNE	-0.03	0.40	-0.08	0.93
β_{10} :regionS	0.32	0.32	1.00	0.32
β_{11} :regionW	2.49	0.42	5.91	0.00
β_{12} :log.per.cap.land.area:regionNE	-0.01	0.01	-0.88	0.38
β_{13} :log.per.cap.land.area:regionS	0.01	0.01	1.19	0.24
β_{14} :log.per.cap.land.area:regionW	0.03	0.01	2.23	0.03
β_{15} :log.per.cap.doctors:regionNE	0.01	0.03	0.23	0.82
β_{16} :log.per.cap.doctors:regionS	0.03	0.02	1.46	0.15
β_{17} :log.per.cap.doctors:regionW	0.12	0.03	3.98	0.00
β_{18} :pct.hs.grad:regionNE	0.00	0.00	0.43	0.67
β_{19} :pct.hs.grad:regionS	0.00	0.00	0.04	0.96
β_{20} :pct.hs.grad:regionW	-0.02	0.00	-4.59	0.00
β_{21} :pct.below.pov:regionNE	0.00	0.01	-0.89	0.38
β_{22} :pct.below.pov:regionS	0.00	0.00	0.78	0.44
β_{23} :pct.below.pov:regionW	-0.02	0.01	-3.54	0.00
β_{24} :pct.unemp:regionNE	-0.01	0.01	-1.30	0.19
β_{25} :pct.unemp:regionS	-0.02	0.01	-2.64	0.01
β_{26} :pct.unemp:regionW	-0.02	0.01	-2.51	0.01

Table 5: Estimated coefficients for model(8).

	df	AIC	BIC
all.subsets.final.model	10	-940.5743	-899.7065
stepwise.bic	10	-940.5743	-899.7065
stepwise.aic	11	-942.0976	-897.1431
stepwise.bic.2-way-inter	16	-1047.7658	-982.3774
stepwise.aic.2-way-inter	23	-1082.1848	-988.1890

Table 6: Models Comparison with AIC and BIC.

The last variable selection method we'll consider is the LASSO. And there is not such an obvious place to cut the shrinkage plot (Figure 7 in Appendix 4, pg.25), to help determine what variables should be kept in the model. Using cross-valiation, we got the model which minimizes 10-fold cross-validation error contains all 10 predictors. The model 9 that is 1 SE has 2 less variable than the model that we first saw with all-subsets regression.

$$\begin{aligned}\log(per.cap.incom) =& \beta_0 + \beta_1 * log(per.cap.land.area) + \beta_2 * pop.18\_34 \\ &+ \beta_4 * log(per.cap.doctors) + \beta_5 * pct.hs.grad \\ &+ \beta_6 * pct.bach.deg + \beta_7 * pct.below.pov \\ &+ \beta_8 * pct.unemp\end{aligned} \tag{9}$$

Though F-test prefers the model that is 1 SE based on LASSO, both AIC and BIC prefers the original model based on the all-subsets regression (Appendix 5, pg.24). So for better interpretation and the integrality of the model, we will settle on the very first model 8 we got based on the all-subsets regression.

5 Discussion

Though in the initial exploratory data analysis, we did not see severe skewness in per ca-pita income, however, we still consider logarithms transformation for per ca-pita income. There is because we can explain the logarithms in terms of percent-change concepts, which makes the model easier to be understood.

From the correlation plot (See Figure 2), it is clear that several variables are highly correlated with each other. Then correlations came in a group of five and were all positively correlated with each other, which consist of crimes, population, total income, doctors and hospital beds. A reasonable person would expect a strong correlation between total income and population and between population and crimes. And larger population also means more medical resources, indicating higher number of doctors and hospital beds, which are also highly correlated.

Besides, the percent of population that have high school degree are negatively correlated with the percent of population that are below poverty level, implying the those graduates from high school are less likely to be in poverty in the future. And it is natural to say that if the percent of population aged 18–34 in a county is higher, the the percent of population aged 65 or older is lower.

That is just common sense that higher education leads to higher income, which is also proved in later regression analysis. This explains why the percent of population have bachelor's degree, the percent of population that have high school degree and per capita income, are moderately positively correlated with each other. And maybe we could say people who have high school degree are more likely to go to pursues her/his bachelor's degree.

When comparing total crimes and and crime rate to predict per capita income, total crimes seems to be a better option. However, it is not convincing enough, since: 1) every county has different population, which may influence the total crimes; 2) per capita crime is more comparable to, or at least on the same scale as, per capita income. Thus, we settled on the model using crime rate with region included. And the region of the United States where the county resides in is likely to have an impact on per capita income.

In our regression analysis, average per capita income is positively correlated with per capita doctors in a county and the percent of the population that have a bachelor's degree. All make perfect sense, since doctors are well-paid jobs, and higher education usually means higher income. Average per capita income is negatively correlated with county's per capita land area, the percent of the population aged 18-34 and the percent of percent below poverty level. We might conjecture that this is because 18-34 year old are not at peak earning capacity yet and so perhaps their lower incomes drags down the per capita average.

Overall, the percent of the population that are high school graduates doesn't have much effect, except in the West. Though, we did not have a very good explanation for this, and the same story is for the percent of the population that are 65 years old and over.

As discussed above, our results are basically consistent with common sense. More job opportunities, more well-paid jobs, higher education and better social well-being are essential for increasing average

per capita income in a county. The composition of population has some effects on average per capita income in a county, but this mostly is due to the income gap between various populations. Since we also took regions into consideration, it shows in our analysis that in several of the interactions for region, the West shows up as deviating significantly from the North Central part of the US.

To address the final question about missing counties in the data set, it should be a bit worrying that we did not consider them into the model. Our study is limited since the data only covers 373 counties, and it would be very useful to have additional data to compare some of the models we found. Since 440 counties that were used in the study are the 440 largest countries in the United States, other 2500 smaller counties are not likely to be representative. That is because smaller counties usually have smaller populations, fewer medical resources, fewer educational resources and different population composition. Instead, in a more complete data set, the data from the 440 largest counties might even become outliers. And this definitely needs further research.

We are using reasonable methods for variable selection, but since it is all within-sample, which means our entire data set is our training sample, there is ample room for over fitting noise in the data. Moreover, some of our inferences about which variables to leave in or take out may be based on overly optimistic standard error estimates. For example, the coefficient on percent unemployment seems to go the wrong way, and the coefficient on percent high school graduates is quite small, statistically and practically (it remains in the model because there is a noticeable interaction that it participates in). If we were able to cross-validate on some new or hold-out data, we might be able to better distinguish what the best model is, because we are able to analyze prediction error. Besides, the fact that stepwise regression found some well-fitting models with interactions between continuous variables suggests exploring those more complex models in the future.

Also just to simplify our analysis, we did not explore the state variable at all. Some of the relationship between these demographic variables and per capita income might be explainable in terms of varying economic policy from one state to another.

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Appendix

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Appendix 1. Initial Data Exploration & Transformation

Read the data in, get a general sense of the variables, and make a "pairs" plot (scatterplot matrix) of the numerical variables.

```
# loading the needed packages
library(Hmisc)
library(arm)
library(corrplot)
library(dplyr)
library(car)
library(alr3)
library(MASS)
library(leaps)
library(glmnet)
library(tidyverse)
library(kableExtra)
library(GGally)
library(grid)
library(gridExtra)
library(ggplotify)
library(reshape2)
```

```
cdi <- read.table("cdi.dat") %>% data.frame()

# Check to see how many unique values each variable has
apply(cdi,2,function(x) {length(unique(x))}) %>%
  kbl(booktabs=T,col.names="unique values",caption=" ") %>%
  kable_classic(full_width=F)
```

Table 1:

	unique values
id	440
county	373
state	48
land.area	384
pop	440
pop.18_34	149
pop.65_plus	137
doctors	360
hosp.beds	391
crimes	437
pct.hs.grad	223
pct.bach.deg	220
pct.below.pov	155
pct.unemp	97
per.cap.income	436
tot.income	428
region	4

There are two category of variables in data, we divided them into numeric and categorical variables for a more refined look.

```
cdinumeric <- cdi[,-c(1,2,3,17)]

# Summary Statistics for Numeric Variables
apply(cdinumeric,2,function(x){c(summary(x),SD=sd(x))}) %>% as.data.frame %>% t() %>%
  round(digits=2) %>% kbl(booktabs=T,caption=" ") %>% kable_classic()
```

There are several variables with Mean substantially larger than Median (`land.area`, `pop`, `doctors`, `hosp.beds`, `crimes`, `per.cap.income`, and `total.income`), indicating possible right-skewing.

```
tmp <- rbind(with(cdi,table(region)))
row.names(tmp) <- "Freq"

# Summary Statistics for Character Variables (Region) which we will be using
tmp %>% kbl(booktabs=T,caption=" ") %>% kable_classic(full_width=F)
```

Then, we will look at the variables with a scatterplot matrix and histograms for each variable.

Univariable distributions:

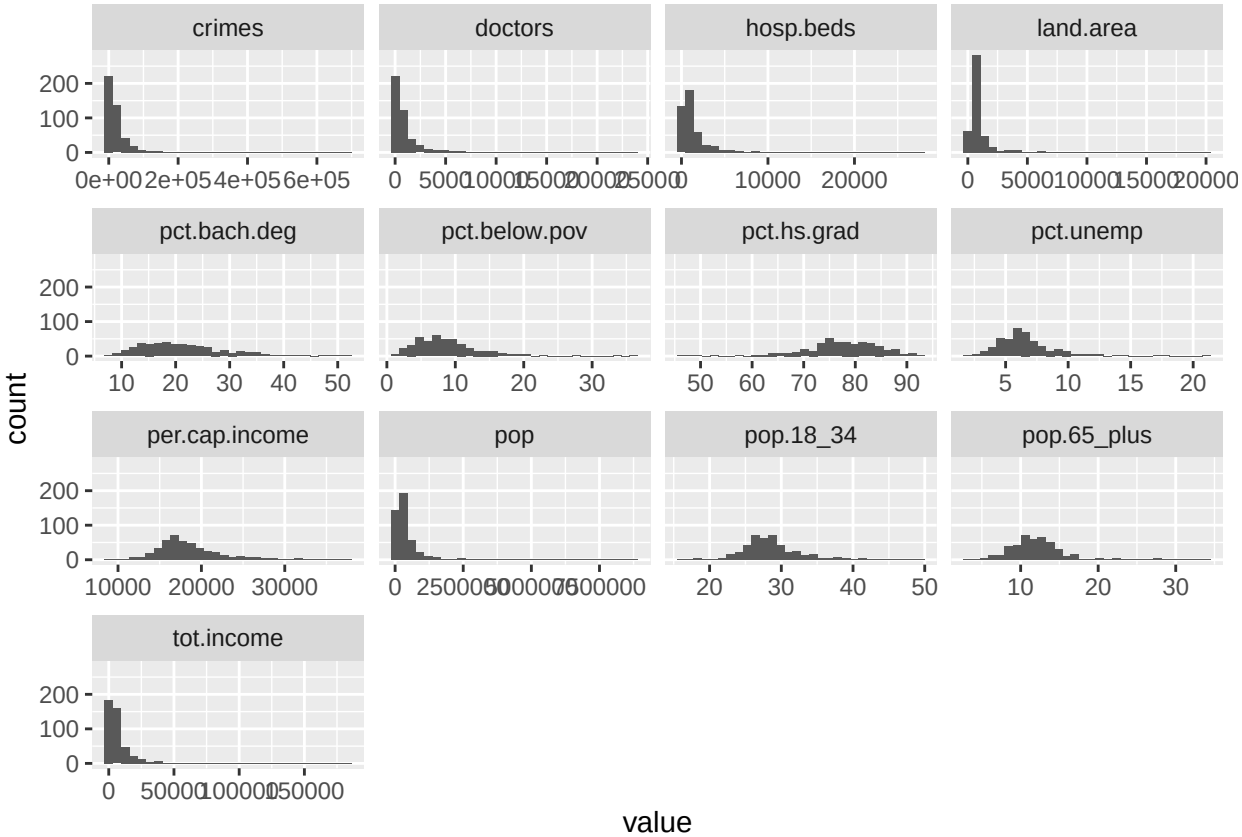
```
# histograms for all numeric predictor variables
ggplot(gather(cdinumeric), aes(value)) +
    geom_histogram(bins = 30) +
  facet_wrap(~key, scales = 'free_x')
```

Table 2:

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	SD
land.area	15.0	451.25	656.50	1041.41	946.75	20062.0	1549.92
pop	100043.0	139027.25	217280.50	393010.92	436064.50	8863164.0	601987.02
pop.18_34	16.4	26.20	28.10	28.57	30.02	49.7	4.19
pop.65_plus	3.0	9.88	11.75	12.17	13.62	33.8	3.99
doctors	39.0	182.75	401.00	988.00	1036.00	23677.0	1789.75
hosp.beds	92.0	390.75	755.00	1458.63	1575.75	27700.0	2289.13
crimes	563.0	6219.50	11820.50	27111.62	26279.50	688936.0	58237.51
pct.hs.grad	46.6	73.88	77.70	77.56	82.40	92.9	7.02
pct.bach.deg	8.1	15.28	19.70	21.08	25.33	52.3	7.65
pct.below.pov	1.4	5.30	7.90	8.72	10.90	36.3	4.66
pct.unemp	2.2	5.10	6.20	6.60	7.50	21.3	2.34
per.cap.income	8899.0	16118.25	17759.00	18561.48	20270.00	37541.0	4059.19
tot.income	1141.0	2311.00	3857.00	7869.27	8654.25	184230.0	12884.32

Table 3:

	NC	NE	S	W
Freq	108	103	152	77



As we can see, `land.area`, `pop`, `tot.income`, `doctors`, `hosp.beds`, `crimes` and maybe `per.cap.income`

are severely skewed, which are the same variables that we identified from above. Thus, we need to consider transformations of the these 7 predictor variables.

Bivariate relationships:

Heatmap of the correlation matrix with a large number of variables

```
co <- cor(cdinumeric)
corrplot::corrplot(co, order = "hclust", tl.col="black")
```

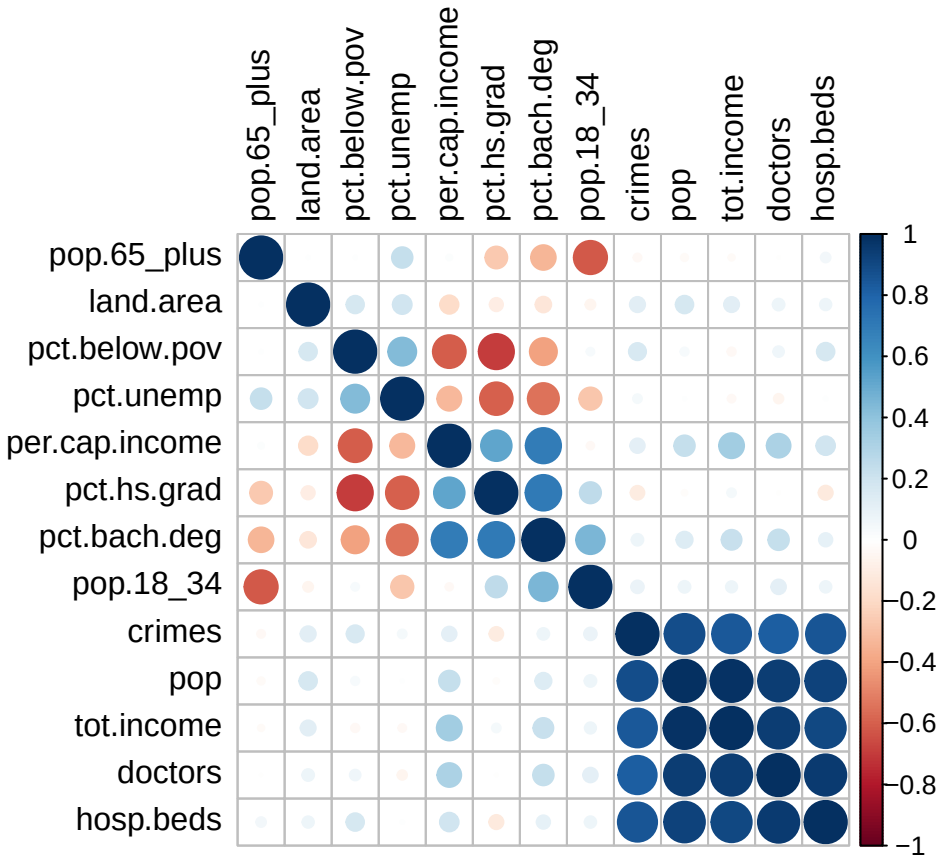


Figure 1: Heat Map of Correlatons Among Variables

The correlation plot suggests that we may run into multi-collinearity problems. Now, we will look at the scatterplot matrix of the data.

```
# make a plot with all predictor variables
cdi2 <- data.frame(cdinumeric, region=cdi$region)

# scatter plots with `per.cap.income`
scatter.builder <- function(df,yvar="per.cap.income") {
    result <- NULL
    y.index <- grep(yvar,names(df))
    for (xvar in names(df)[-y.index]) {
      d <- data.frame(xx=df[,xvar],yy=df[,y.index])
      if(mode(df[,xvar])=="numeric") {
        p <- ggplot(d,aes(x=xx,y=yy)) + geom_point() +
```

```
                ggtitle("") + xlab(xvar) + ylab(yvar)
      } else {
          p <- ggplot(d,aes(x=xx,y=yy)) + geom_boxplot(notch=F) +
                ggtitle("") + xlab(xvar) + ylab(yvar)
      }
    result <- c(result,list(p))
    }
    return(result)
}

grid.arrange(grobs=scatter.builder(cdi2))
```

We are going to take the logarithms of the variables that we identified earlier, to address heavy skewing and potential leverage and influence issues. The reason for using logarithms is that the transformed variables can be explained to the social scientist in terms of percent-change concepts.

```
cdilogs <- cdi2

skewed.vars <- c("land.area", "pop", "doctors", "hosp.beds", "crimes", "tot.income", "per.cap.income")

for (tmp in skewed.vars) {
  loc <- grep(paste("^",tmp,"$",sep=""),names(cdilogs))
  cdilogs[,loc] <- log(cdilogs[,loc])
  names(cdilogs)[loc] <- paste("log.",names(cdilogs)[loc],sep="")
}
```

Then, we start fitting the first model.

```
# regression
fit <- lm(per.cap.income ~ ., data = cdi2)
summary(fit)
```

```
##
## Call:
## lm(formula = per.cap.income ~ ., data = cdi2)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -7592.2  -879.1   -67.3   763.8  7714.8
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2.887e+04  2.107e+03  13.703  < 2e-16 ***
## land.area      7.795e-02  6.267e-02   1.244 0.214279
## pop           -1.689e-02  1.364e-03 -12.377  < 2e-16 ***
## pop.18_34     -2.525e+02  2.640e+01  -9.566  < 2e-16 ***
## pop.65_plus   -3.430e+01  2.635e+01  -1.302 0.193646
## doctors       -5.458e-01  2.175e-01  -2.509 0.012464 *
## hosp.beds      9.254e-01  1.522e-01   6.081 2.67e-09 ***
## crimes         1.082e-02  3.273e-03   3.307 0.001025 **
## pct.hs.grad   -1.107e+02  2.352e+01  -4.708 3.40e-06 ***
## pct.bach.deg   3.624e+02  1.975e+01  18.347  < 2e-16 ***
```

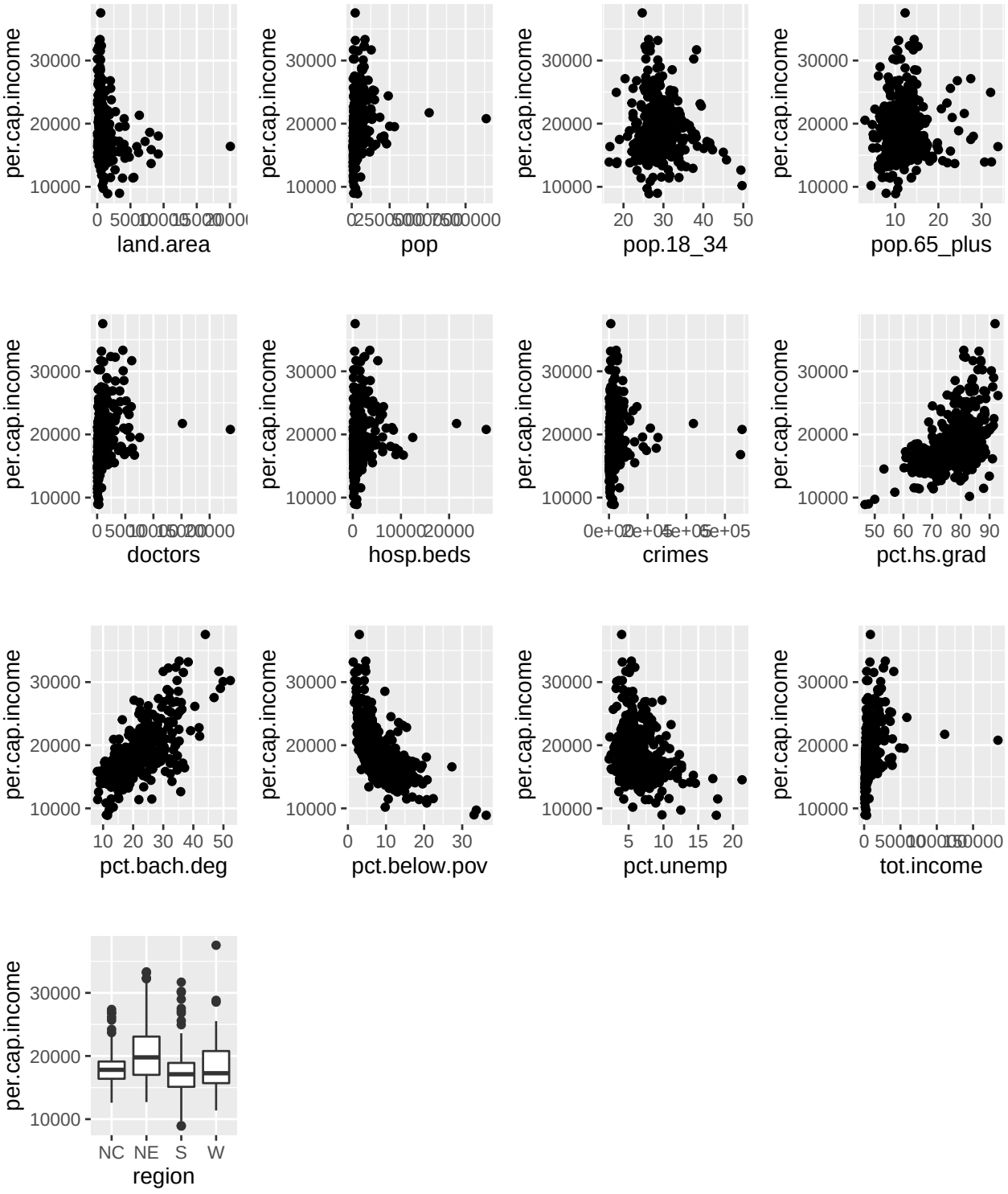
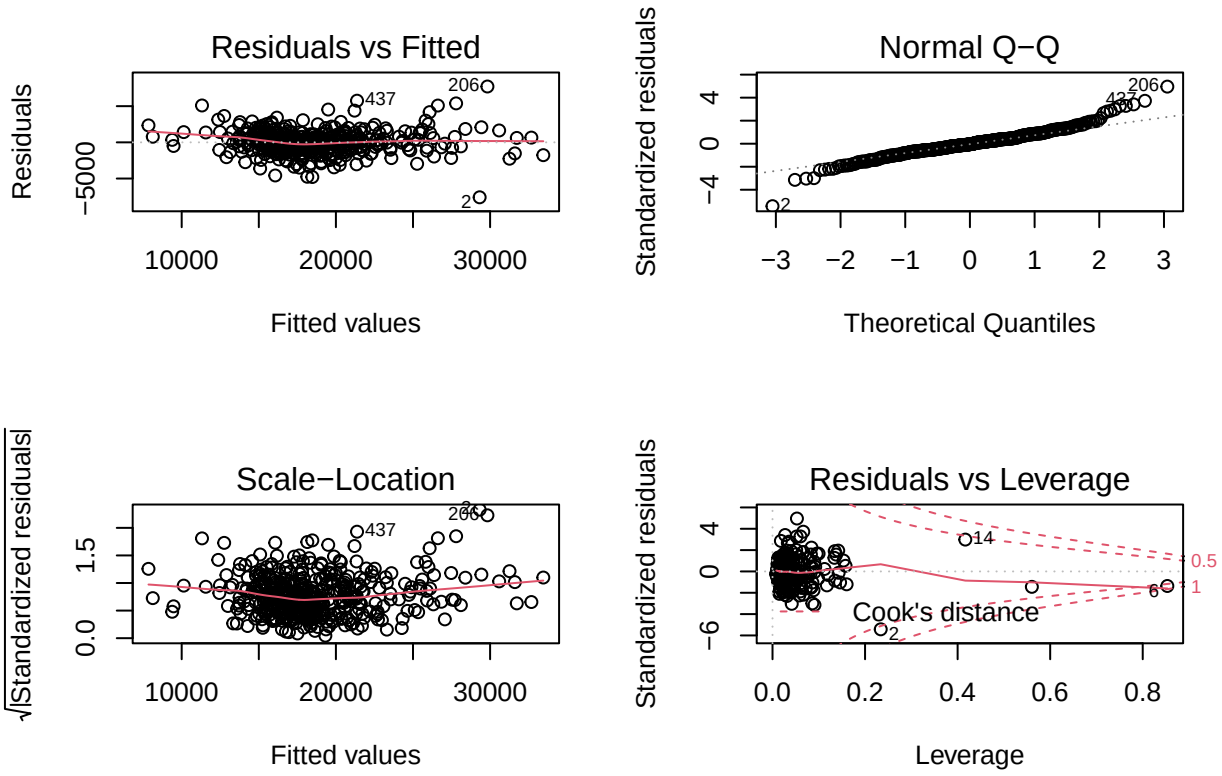


Figure 2: Scatter Plots with y = per.cap.income

```
## pct.below.pov -3.380e+02  2.945e+01 -11.479  < 2e-16 ***
## pct.unemp      1.631e+02  4.606e+01   3.542 0.000441 ***
## tot.income     7.251e-01  5.921e-02  12.246  < 2e-16 ***
## regionNE       2.461e+02  2.432e+02   1.012 0.312099
## regionS       -3.727e+02  2.292e+02  -1.626 0.104739
## regionW       -2.157e+02  2.875e+02  -0.750 0.453528
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1598 on 424 degrees of freedom
## Multiple R-squared:  0.8502, Adjusted R-squared:  0.8449
## F-statistic: 160.5 on 15 and 424 DF,  p-value: < 2.2e-16
```

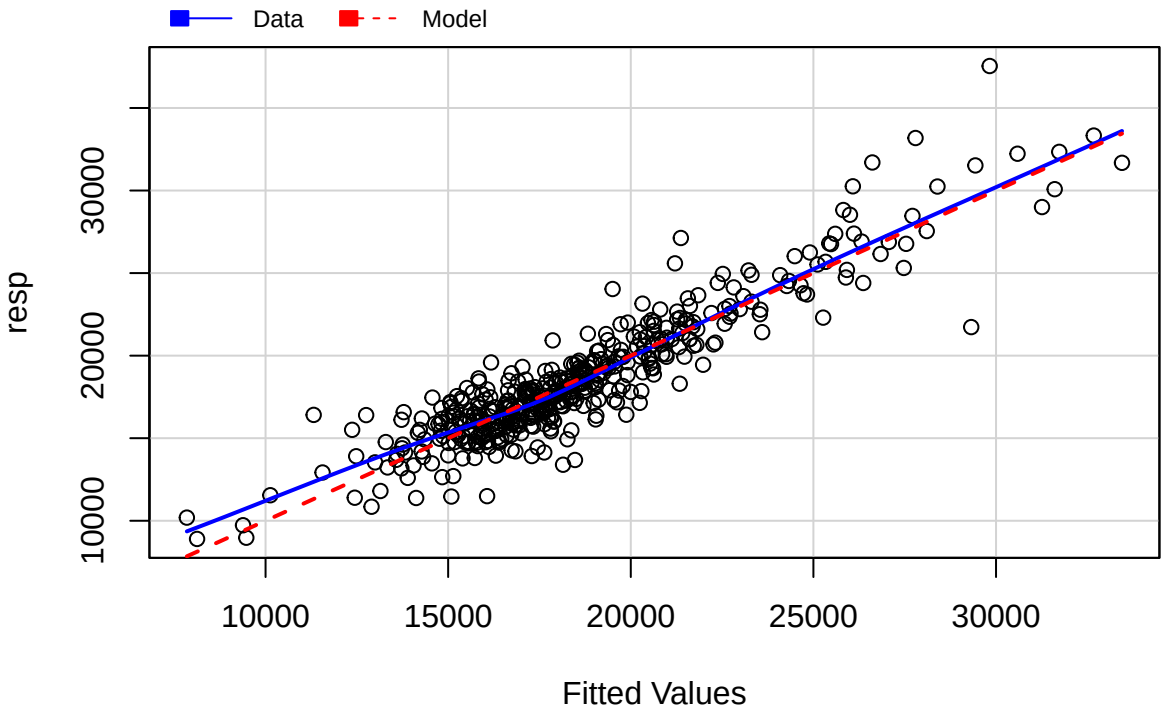
Then, we will check the diagnostic plots

```
par(mfrow=c(2,2))
plot(fit)
```



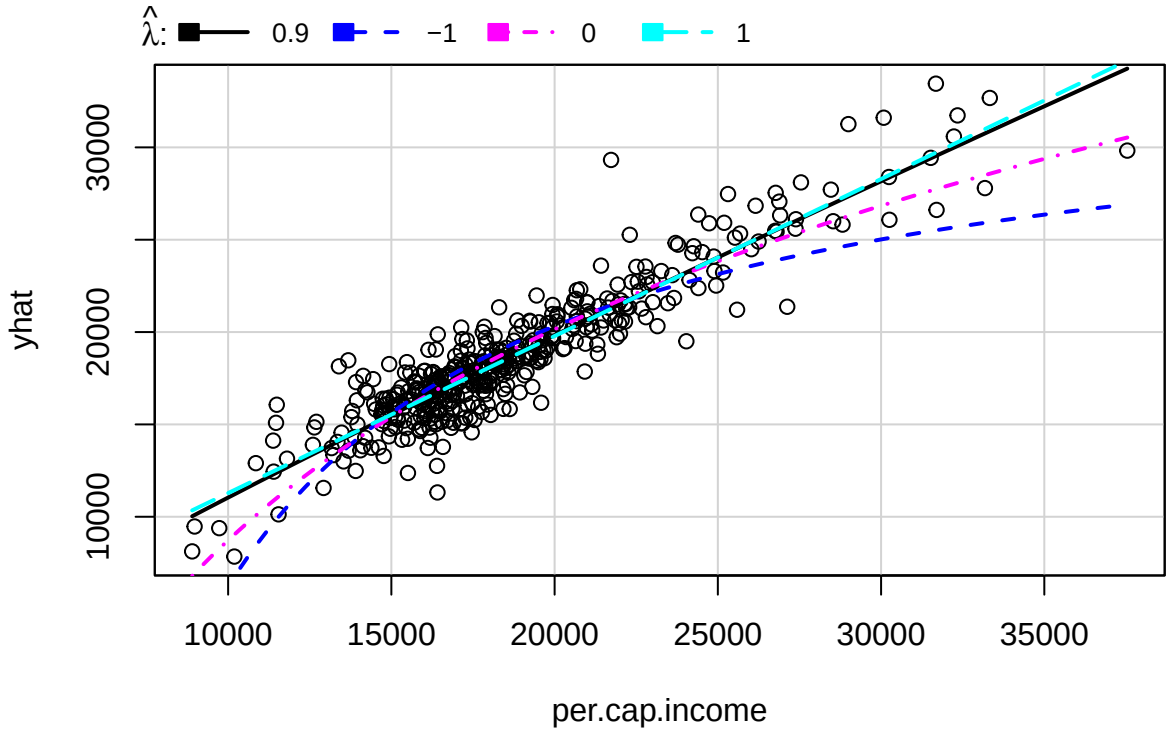
Both summary and the diagnostic plots look pretty great, except a little concave in standardized residuals against fitted value.

```
# marginal model plot for y and fitted values
par(mfrow=c(1,1))
m1 <- lm(cdi2$per.cap.income~fit$fitted.values)
mmp(m1,fit$fitted.values,xlab="Fitted Values",key=NULL)
```



The marginal model plot for y and fitted values looks good, though there is departure in the left tail. Thus, we also consider transformation for `per.cap.income`.

```
# inverse response plot for the data
inverseResponsePlot(fit,key=TRUE)
```




```
##        lambda         RSS
```

```
## 1  0.8997968  919453119
## 2 -1.0000000 1511669678
## 3  0.0000000 1051021057
## 4  1.0000000  921021431
```

As we can see in the plot, $\lambda = 0$, which corresponds to natural logarithms provides a very good fit, as its fitted line is very close the optimal $\lambda = -0.11$'s. Thus, for better interpretation of the model, we choose natural logarithm transformation for y.

Let's check the transformed data.

```
# histogram of transformed data
hist.builder <- function(df) {  ## creates a list of graphs
    result <- NULL
    for (var in names(df)) {
      d <- data.frame(dd=df[,var])
      if(mode(df[,var])=="numeric") {
        p <- ggplot(d,aes(x=dd)) + geom_histogram(bins = 30) +
               ggtitle(var) + xlab("")
      } else {
          p <- ggplot(d,aes(x=dd)) + geom_bar() +
                 ggtitle(var) + xlab("")
      }
    result <- c(result,list(p))
    }
    return(result)
}

grid.arrange(grobs=hist.builder(cdilogs))
```

```
# Correlations after log transformations
co <- cor(cdilogs[,-grep("region",names(cdilogs))])
corrplot::corrplot(co, order = "hclust", tl.col="black")
```

```
# Scatterplots after log transformations
grid.arrange(grobs=scatter.builder(cdilogs,"log.per.cap.income"))
```

Except for `log.pop`, the skewing seems to have largely been brought under control.

Appendix 2. Analysis of Relationship between Per ca-pita income and Crime Rate

For log.per.cap.income and log.crimes, the six models to consider are:

```
ancova.01 <- lm(log.per.cap.income ~ log.crimes,data=cdilogs)

ancova.02 <- lm(log.per.cap.income ~ log.crimes + region,data=cdilogs)

ancova.03 <- lm(log.per.cap.income ~ log.crimes * region,data=cdilogs)
```

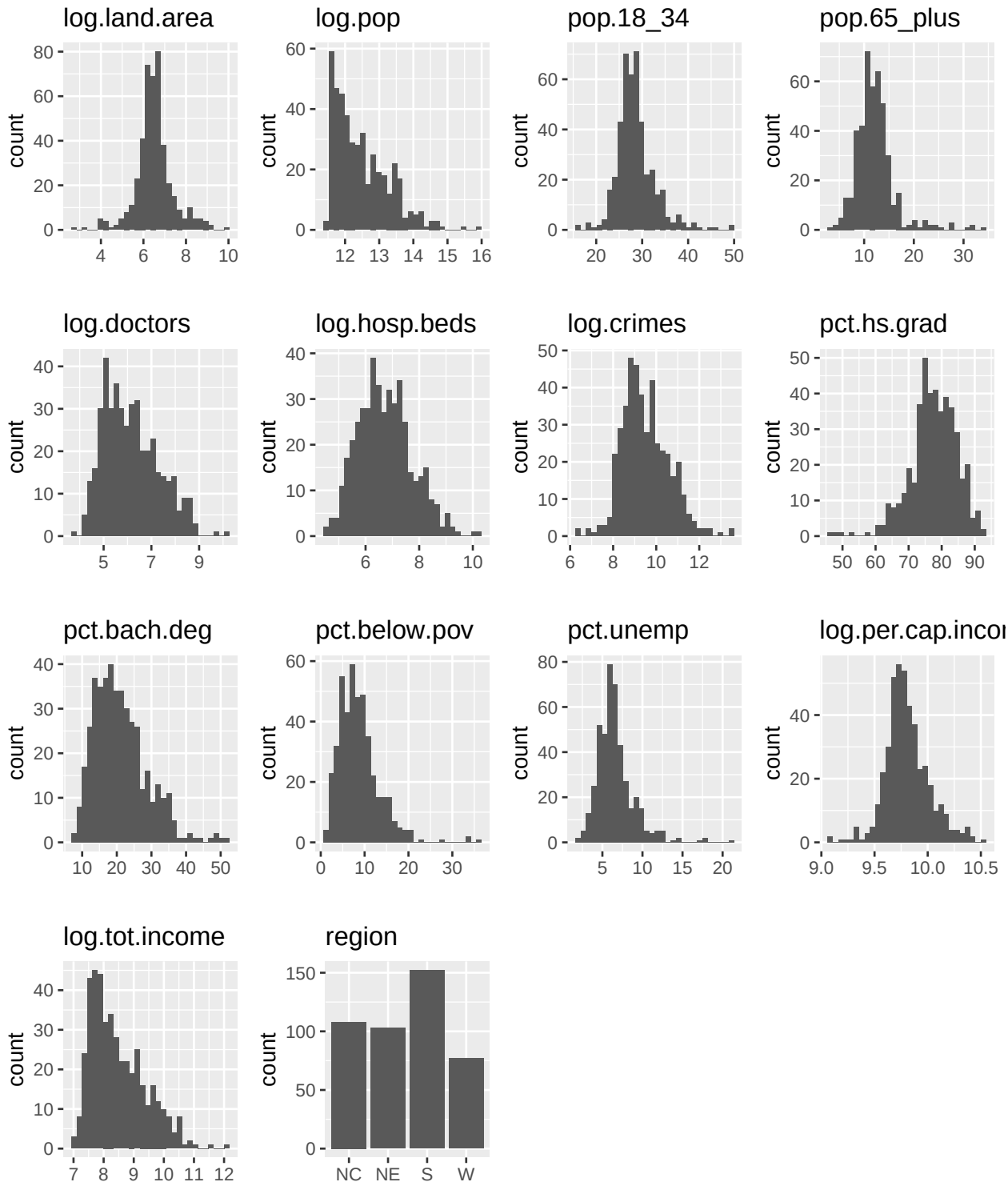


Figure 3: Histograms after log transformations

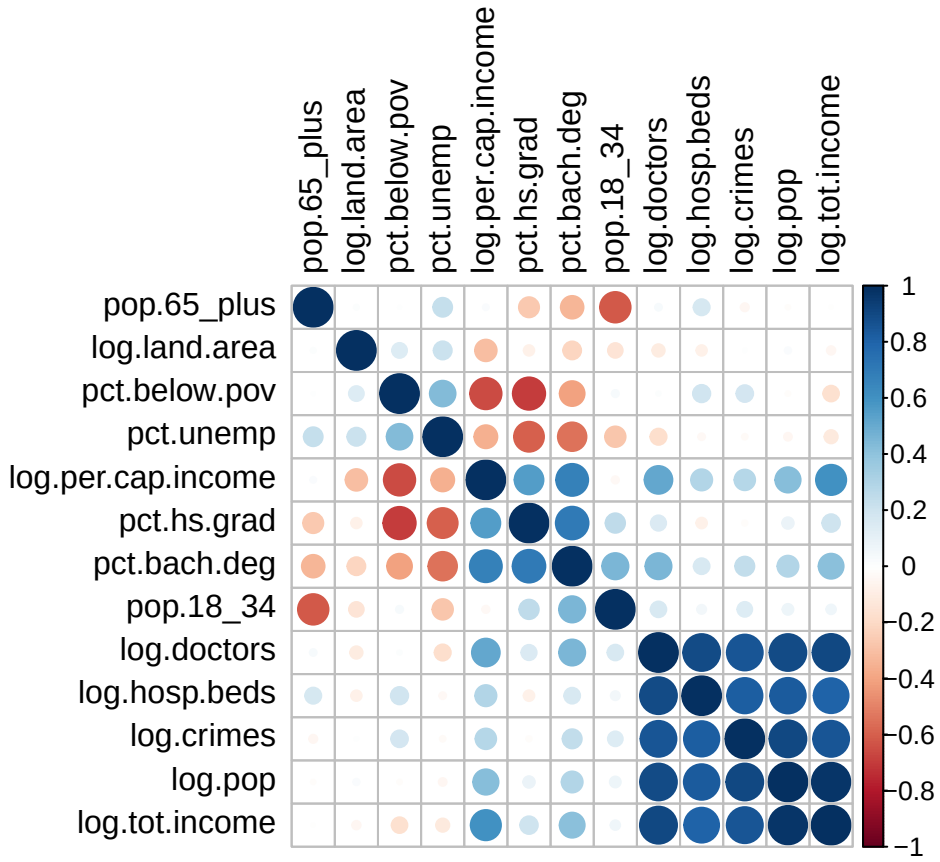


Figure 4: Correlations after log transformations

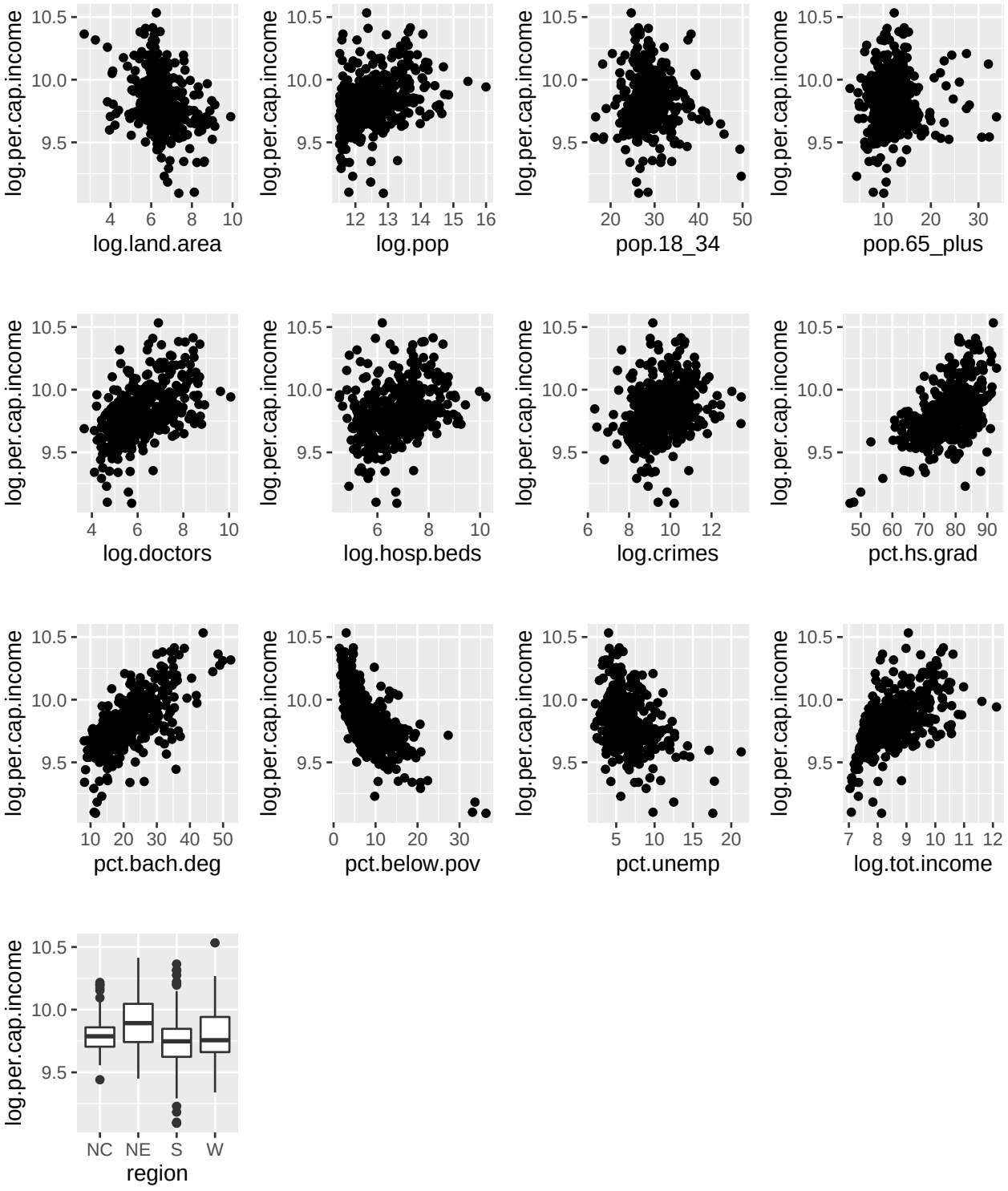


Figure 5: Scatterplots after log transformations

	df	AIC	BIC
ancova.01	3	-169.9466	-157.6863
ancova.02	6	-227.4746	-202.9539
ancova.03	9	-223.7402	-186.9593
ancova.04	3	-135.0340	-122.7737
ancova.05	6	-172.1347	-147.6140
ancova.06	9	-166.7601	-129.9792

```
# regression model with per-capita crime
attach(cdi2)
log.per.cap.crimes <-log(crimes) - log(pop)
detach()

ancova.04 <- lm(log.per.cap.income ~ log.per.cap.crimes,data=cdilogs)

ancova.05 <- lm(log.per.cap.income ~ log.per.cap.crimes + region,data=cdilogs)

ancova.06 <- lm(log.per.cap.income ~ log.per.cap.crimes * region,data=cdilogs)
```

We could compare all 6 models with AIC or BIC. In this case, we get the same result: the additive model ancova.02 has both the lowest AIC and the lowest BIC values.

```
# table comparing all 6 models with AIC or BIC
data.frame(AIC=AIC(ancova.01,ancova.02,ancova.03,ancova.04,ancova.05,ancova.06),
BIC=BIC(ancova.01,ancova.02,ancova.03,ancova.04,ancova.05,ancova.06))[,-3] %>%
  kbl(booktabs=T,col.names=c("df","AIC","BIC")) %>% kable_classic(full_width=F)
```

However, there is an argument that per-capita crime is more comparable to, or at least on the same scale as, per-capita income, so we will briefly look at the second-best model, model 5 (anova.05), to see how it compares to model 2 (ancova.02):

```
oldmar <- par()$mar

par(mfrow=c(2,4))

par(mar=c(2,2,2,2))

invisible(lapply(list(ancova.02,ancova.05),
                 function(x) plot(x,cex.main=0.5)))
```

```
par(mar=oldmar)
```

Both the diagnostic plots don't show much, except that the QQ plot suggests both the left and the right tails are a bit longer than expected for the normal distribution. Thus, for better interpretation, we finally decide on the model 5.

```
formula(ancova.05)
```

```
## log.per.cap.income ~ log.per.cap.crimes + region
```

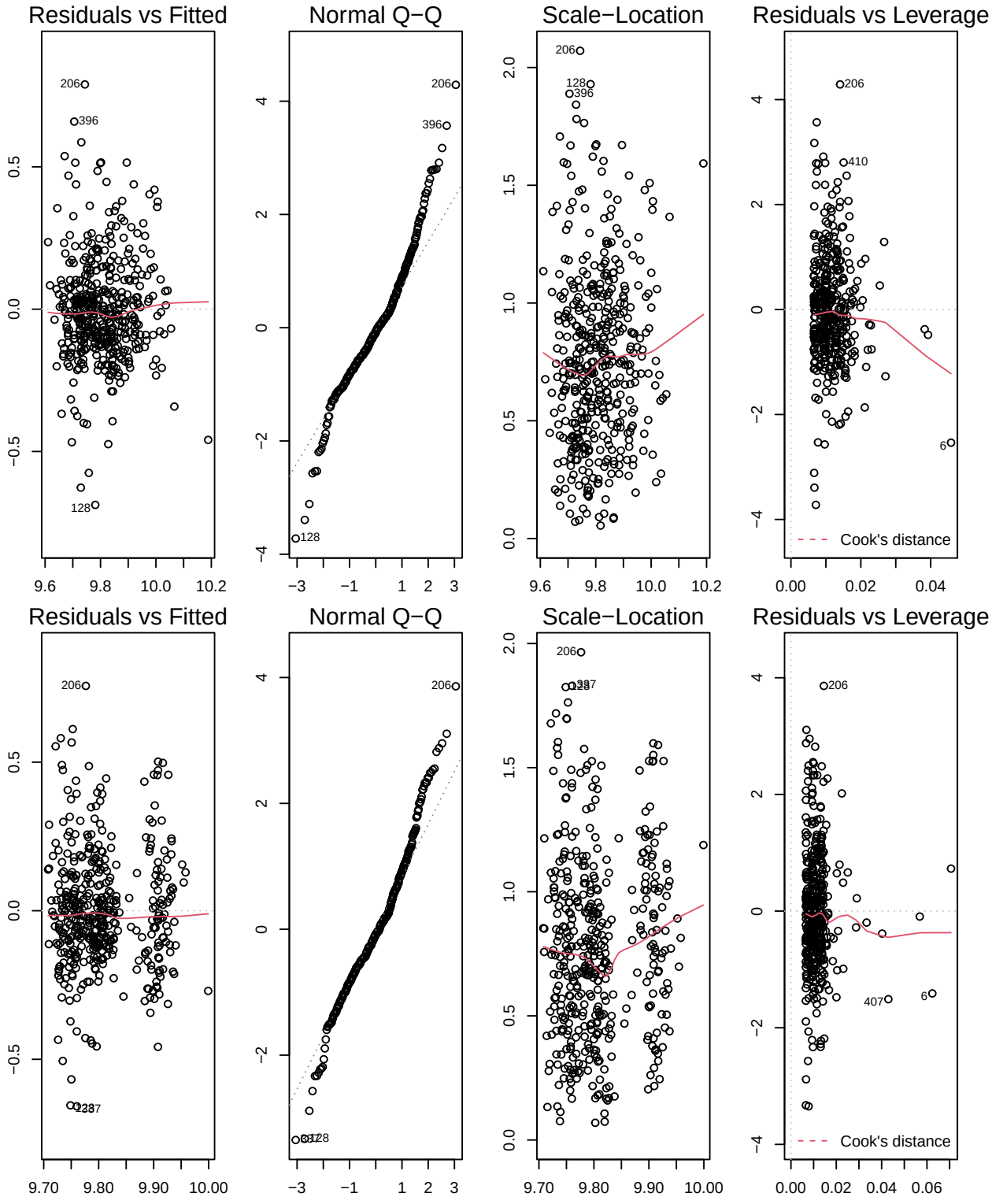


Figure 6: Residual diagnostics for all 2 ANCOVA models, in order: ancova.02, ancova.05

```
round(coef(summary(ancova.05)),2)
```

```
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)             9.94       0.07  143.30     0.00
## log.per.cap.crimes      0.04       0.02    1.98     0.05
## regionNE                0.11       0.03    4.15     0.00
## regionS                -0.07       0.03   -2.84     0.00
## regionW                -0.02       0.03   -0.81     0.42
```

Appendix 3. Regression Analysis – All Subsets(without Regions)

Per-capita variables are more comparable to, or at least on the same scale as, per-capita income. So, we will convert land area, doctors, hospital beds, crimes and total income into per ca-pita scales.

```
# conversion for the data
cdiperlogs <- cdi2

loc <- grep(paste("^","pop","$",sep=""), names(cdiperlogs))
cdiperlogs[,loc] <- log(cdiperlogs[,loc])
names(cdiperlogs)[loc] <- paste("log.",names(cdiperlogs)[loc],sep="")

loc <- grep(paste("^", "per.cap.income","$",sep=""), names(cdiperlogs))
cdiperlogs[,loc] <- log(cdiperlogs[,loc])
names(cdiperlogs)[loc] <- paste("log.",names(cdiperlogs)[loc],sep="")

vars <- c("land.area", "doctors", "hosp.beds", "crimes", "tot.income")

for (tmp in skewed.vars) {
  loc <- grep(paste("^",tmp,"$",sep=""),names(cdiperlogs))
  cdiperlogs[,loc] <- log(cdiperlogs[,loc]) - cdilogs$log.pop
  names(cdiperlogs)[loc] <- paste("log.per.cap.",names(cdiperlogs)[loc],sep="")
}

# take log.pop and log.tot.income out of consideration
omit <- c(grep("log.pop",names(cdilogs)),grep("log.tot.income",names(cdilogs)))
cdilogred <- cdiperlogs[,-omit]

# First, work *without* the `region` variable
cdilogred.cont <- cdilogred[,-grep("region",names(cdilogred))]
names(cdilogred.cont)
```

```
##  [1] "log.per.cap.land.area" "pop.18_34"             "pop.65_plus"
##  [4] "log.per.cap.doctors"   "log.per.cap.hosp.beds" "log.per.cap.crimes"
##  [7] "pct.hs.grad"           "pct.bach.deg"          "pct.below.pov"
## [10] "pct.unemp"             "log.per.cap.income"
```

By finding the model with the lowest BIC, we found the best model.

```
all.subsets.01 <- regsubsets(log.per.cap.income ~ ., data=cdilogred.cont,nvmax=10)

# coefficients and standard errors for the best model
```

```
all.subsets.01.summary <- summary(all.subsets.01)
best.model <- which.min(all.subsets.01.summary$bic)

tmp <- cdilogred.cont[,all.subsets.01.summary$which[best.model,][-1]]
all.subsets.01.final.model <- lm(log.per.cap.income ~ .,data=tmp)
summary(all.subsets.01.final.model)$coef
```

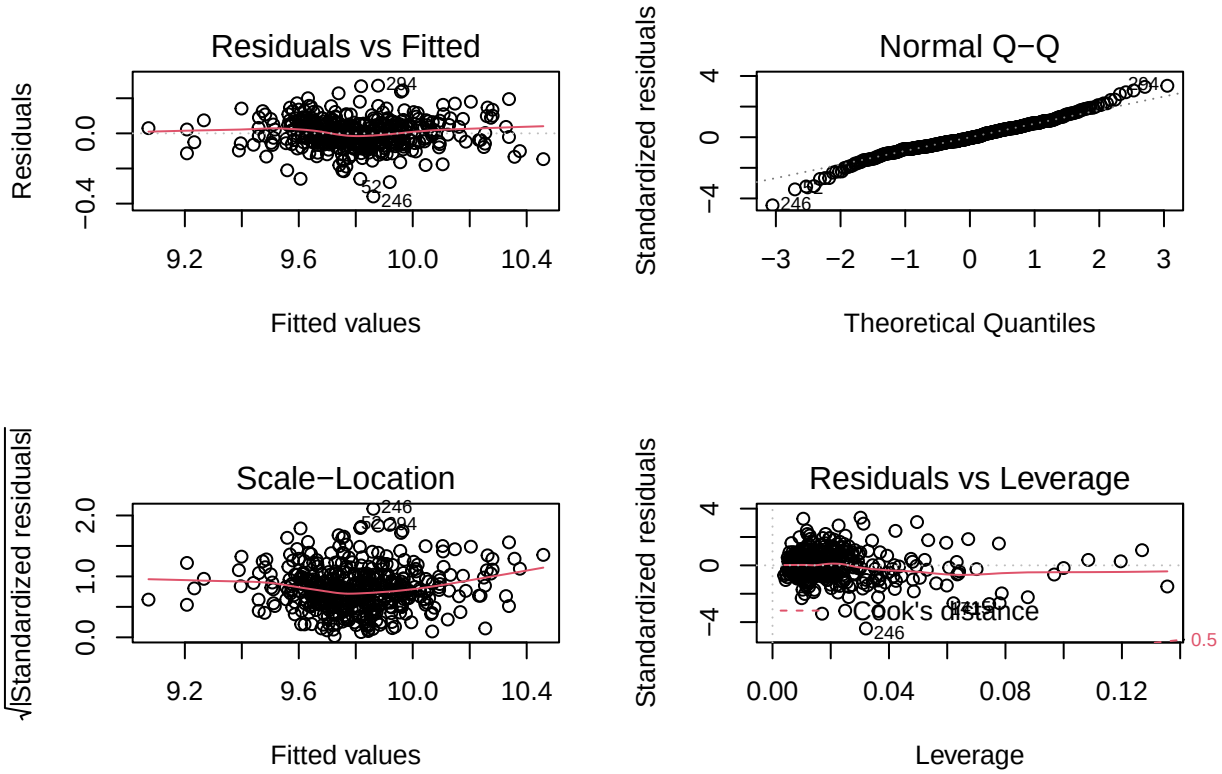
```
##                           Estimate  Std. Error    t value      Pr(>|t|)
## (Intercept)           10.785892327 0.142120643  75.892510 1.623250e-251
## log.per.cap.land.area -0.042512925 0.004017583 -10.581717  2.035599e-23
## pop.18_34             -0.016109168 0.001306346 -12.331471  3.902227e-30
## pop.65_plus           -0.004040904 0.001384429  -2.918824  3.697586e-03
## log.per.cap.doctors    0.087212905 0.010349063   8.427131  5.350058e-16
## pct.hs.grad           -0.004522402 0.001087721  -4.157687  3.880188e-05
## pct.bach.deg           0.014868243 0.000958610  15.510211  1.984929e-43
## pct.below.pov         -0.025183140 0.001329506 -18.941728  1.177048e-58
## pct.unemp              0.012980498 0.002197574   5.906739  7.087581e-09
```

All the predictors have coefficients significantly different from zero. However, most of the coefficients are small, and some seem to have the wrong sign (e.g. `pct.hs.grad` and `pct.unemp`). Next, we will check VIFs and residual diagnostics…

```
vif(all.subsets.01.final.model)
```

```
## log.per.cap.land.area            pop.18_34           pop.65_plus
##              1.417494             1.953668             1.991357
##   log.per.cap.doctors          pct.hs.grad         pct.bach.deg
##              2.159546             3.794826             3.509152
##         pct.below.pov            pct.unemp
##              2.498192             1.720401
```

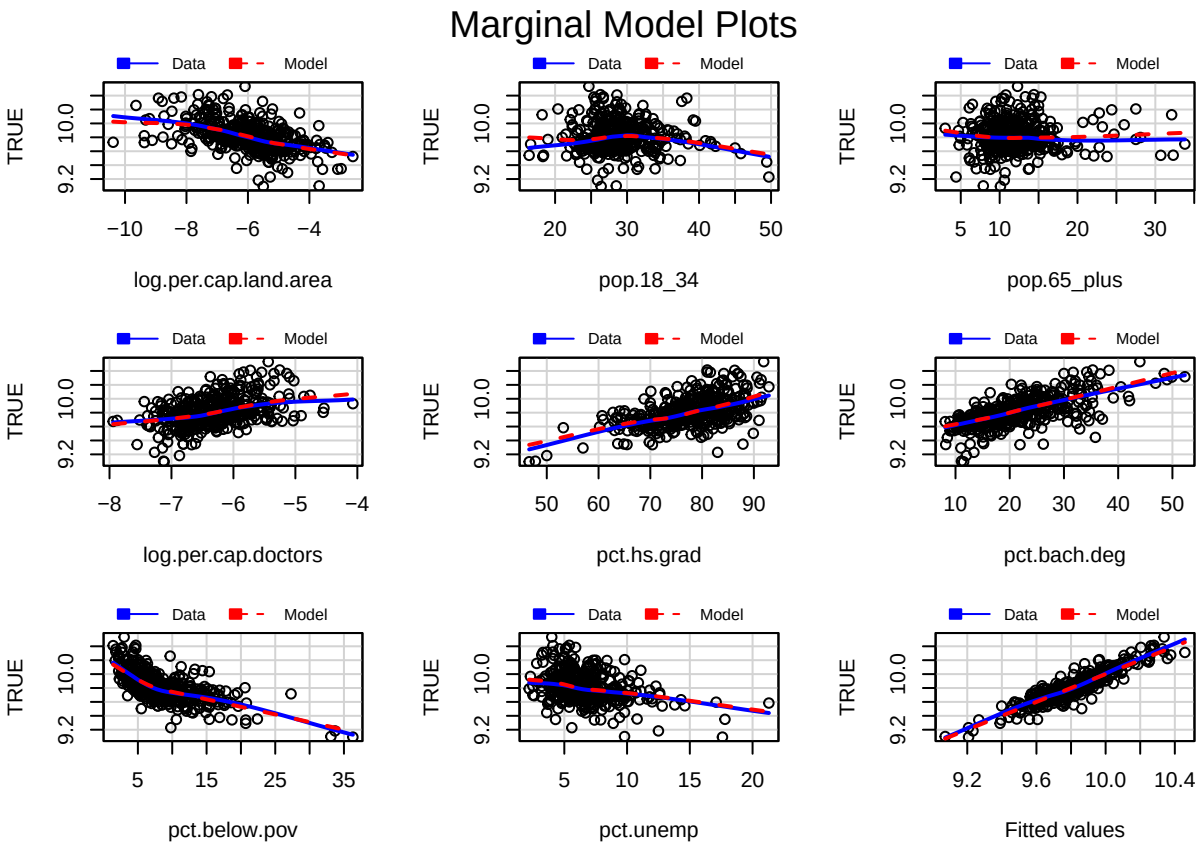
```
par(mfrow=c(2,2))
# diagnostics for the best all subsets model
plot(all.subsets.01.final.model)
```



None of the VIFs seem excessively large, and the diagnostic plots don't show much, except that the QQ plot suggests both the left and the right tails are a bit longer than expected for the normal distribution.

We can also look at marginal model plots, to see if we are missing a transformation, interaction, etc.

```
mmps(all.subsets.01.final.model)
```



The marginal model plots look very good – the blue data-based curves line up well with the red model-based curves.

Appendix 3. Regression Analysis – All Subsets(with Regions)

```
# add regions into regression
tmp <- cbind(tmp,region=cdilogred$region)
all.subsets.01.final.with.region <- lm(log.per.cap.income ~ .*region,data=tmp)
summary(all.subsets.01.final.with.region)
```

```
##
## Call:
## lm(formula = log.per.cap.income ~ . * region, data = tmp)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.243581 -0.043603 -0.000872  0.040701  0.295427
##
## Coefficients:
##                                Estimate Std. Error t value Pr(>|t|)
## (Intercept)                   10.135880   0.375175  27.016  < 2e-16 ***
## log.per.cap.land.area         -0.051212   0.009442  -5.424 1.01e-07 ***
## pop.18_34                     -0.014841   0.002811  -5.279 2.13e-07 ***
## pop.65_plus                    0.001018   0.005243   0.194 0.846093
## log.per.cap.doctors            0.044700   0.018788   2.379 0.017815 *
```

```
## pct.hs.grad                    -0.002202   0.003450  -0.638 0.523774
## pct.bach.deg                    0.014946   0.002924   5.111 4.95e-07 ***
## pct.below.pov                  -0.022998   0.003912  -5.879 8.67e-09 ***
## pct.unemp                       0.018630   0.005028   3.705 0.000241 ***
## regionNE                        0.598161   0.511699   1.169 0.243105
## regionS                         0.317762   0.423040   0.751 0.453006
## regionW                         2.749818   0.561496   4.897 1.41e-06 ***
## log.per.cap.land.area:regionNE  0.002252   0.013452   0.167 0.867157
## log.per.cap.land.area:regionS   0.009275   0.012258   0.757 0.449697
## log.per.cap.land.area:regionW   0.039681   0.013379   2.966 0.003197 **
## pop.18_34:regionNE             -0.006445   0.004235  -1.522 0.128830
## pop.18_34:regionS              -0.001493   0.003409  -0.438 0.661732
## pop.18_34:regionW               0.002727   0.004663   0.585 0.558987
## pop.65_plus:regionNE           -0.009749   0.006618  -1.473 0.141503
## pop.65_plus:regionS            -0.002213   0.005518  -0.401 0.688669
## pop.65_plus:regionW            -0.006832   0.006995  -0.977 0.329256
## log.per.cap.doctors:regionNE    0.009289   0.031949   0.291 0.771392
## log.per.cap.doctors:regionS     0.034939   0.024605   1.420 0.156377
## log.per.cap.doctors:regionW     0.119386   0.037063   3.221 0.001380 **
## pct.hs.grad:regionNE           -0.003461   0.004415  -0.784 0.433613
## pct.hs.grad:regionS             0.001959   0.003807   0.514 0.607216
## pct.hs.grad:regionW            -0.019334   0.004587  -4.215 3.09e-05 ***
## pct.bach.deg:regionNE           0.005030   0.004053   1.241 0.215308
## pct.bach.deg:regionS           -0.002642   0.003201  -0.825 0.409608
## pct.bach.deg:regionW            0.003287   0.003677   0.894 0.371858
## pct.below.pov:regionNE         -0.001206   0.005302  -0.228 0.820138
## pct.below.pov:regionS           0.005633   0.004404   1.279 0.201588
## pct.below.pov:regionW          -0.020050   0.005598  -3.582 0.000383 ***
## pct.unemp:regionNE             -0.007415   0.007575  -0.979 0.328233
## pct.unemp:regionS              -0.022264   0.006929  -3.213 0.001417 **
## pct.unemp:regionW              -0.018451   0.006889  -2.678 0.007699 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.07476 on 404 degrees of freedom
## Multiple R-squared:  0.8797, Adjusted R-squared:  0.8692
## F-statistic: 84.37 on 35 and 404 DF,  p-value: < 2.2e-16
```

Follow a rule of thumb is: if any indicator for a categorical variable seems important (e.g. a statistically significant coefficient), then keep the whole categorical variable. If none of them seem important, then drop the variable. The same thing works for interactions with categorical variables. Thus, the final model will be:

```
all.subsets.01.final.with.some.region <- update(all.subsets.01.final.with.region,
                        . ~ . - region:pop.65_plus - region:pop.18_34 - region:pct.bach.deg)
summary(all.subsets.01.final.with.some.region)
```

```
##
## Call:
## lm(formula = log.per.cap.income ~ log.per.cap.land.area + pop.18_34 +
##     pop.65_plus + log.per.cap.doctors + pct.hs.grad + pct.bach.deg +
##     pct.below.pov + pct.unemp + region + log.per.cap.land.area:region +
##     log.per.cap.doctors:region + pct.hs.grad:region + pct.below.pov:region +
##     pct.unemp:region, data = tmp)
```

```
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.258132 -0.045038 -0.001107  0.040222  0.295175
##
## Coefficients:
##                                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)                    10.2679794  0.2847552  36.059  < 2e-16 ***
## log.per.cap.land.area          -0.0499873  0.0085299  -5.860 9.46e-09 ***
## pop.18_34                      -0.0154108  0.0012915 -11.933  < 2e-16 ***
## pop.65_plus                    -0.0018873  0.0014218  -1.327 0.185117
## log.per.cap.doctors             0.0482811  0.0155591   3.103 0.002047 **
## pct.hs.grad                    -0.0028499  0.0024993  -1.140 0.254832
## pct.bach.deg                    0.0149133  0.0009848  15.143  < 2e-16 ***
## pct.below.pov                  -0.0225437  0.0037358  -6.035 3.55e-09 ***
## pct.unemp                       0.0181418  0.0048832   3.715 0.000231 ***
## regionNE                       -0.0328403  0.3970457  -0.083 0.934121
## regionS                         0.3236732  0.3242043   0.998 0.318689
## regionW                         2.4940100  0.4221170   5.908 7.23e-09 ***
## log.per.cap.land.area:regionNE -0.0104496  0.0118883  -0.879 0.379924
## log.per.cap.land.area:regionS   0.0135607  0.0114089   1.189 0.235280
## log.per.cap.land.area:regionW   0.0268791  0.0120422   2.232 0.026145 *
## log.per.cap.doctors:regionNE    0.0062279  0.0272072   0.229 0.819057
## log.per.cap.doctors:regionS     0.0307224  0.0210523   1.459 0.145233
## log.per.cap.doctors:regionW     0.1193144  0.0299993   3.977 8.23e-05 ***
## pct.hs.grad:regionNE            0.0013270  0.0030688   0.432 0.665654
## pct.hs.grad:regionS             0.0001180  0.0026485   0.045 0.964471
## pct.hs.grad:regionW            -0.0162969  0.0035498  -4.591 5.86e-06 ***
## pct.below.pov:regionNE         -0.0044605  0.0050367  -0.886 0.376340
## pct.below.pov:regionS           0.0032457  0.0041796   0.777 0.437865
## pct.below.pov:regionW          -0.0194333  0.0054923  -3.538 0.000448 ***
## pct.unemp:regionNE             -0.0097674  0.0074850  -1.305 0.192644
## pct.unemp:regionS              -0.0177148  0.0067103  -2.640 0.008606 **
## pct.unemp:regionW              -0.0170169  0.0067854  -2.508 0.012529 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.07595 on 413 degrees of freedom
## Multiple R-squared:  0.873,  Adjusted R-squared:  0.865
## F-statistic: 109.2 on 26 and 413 DF,  p-value: < 2.2e-16
```

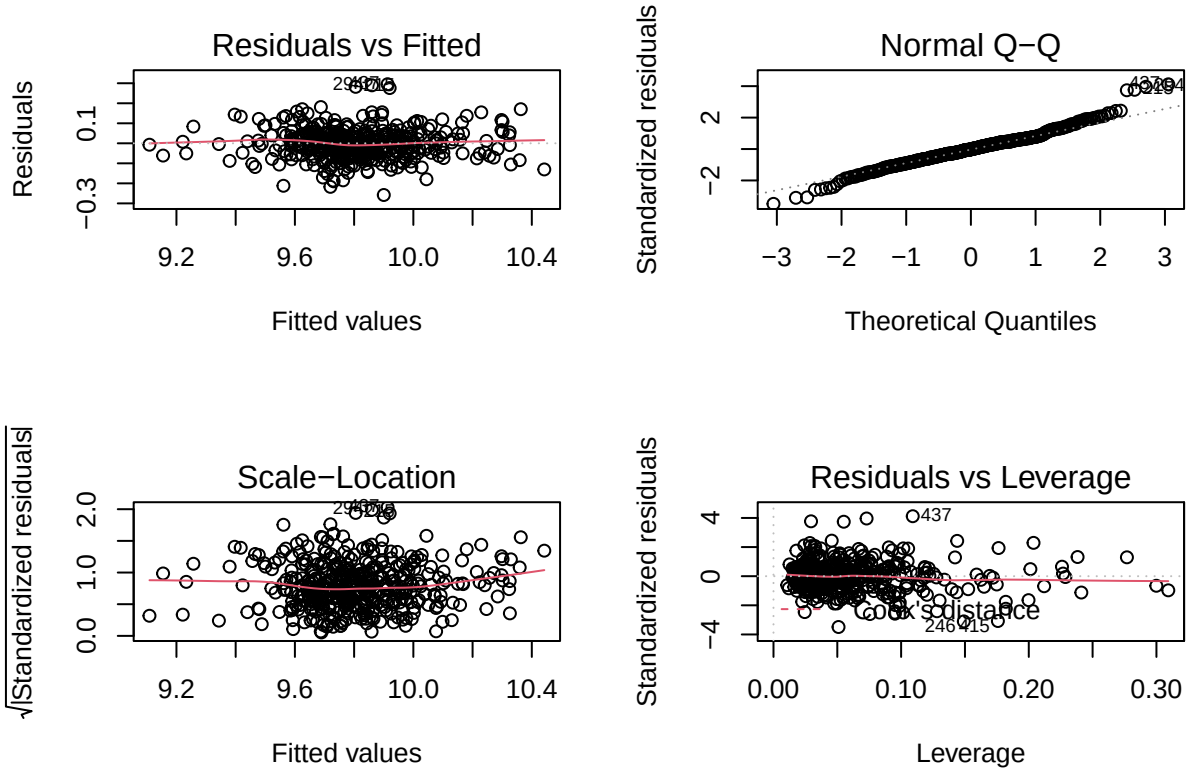
Now, we will quickly check VIFs and diagnostics.

```
vif(all.subsets.01.final.with.some.region)
```

```
##                                    GVIF Df GVIF^(1/(2*Df))
## log.per.cap.land.area       7.460742e+00  1        2.731436
## pop.18_34                   2.229411e+00  1        1.493121
## pop.65_plus                 2.452456e+00  1        1.566032
## log.per.cap.doctors         5.699395e+00  1        2.387341
## pct.hs.grad                 2.339401e+01  1        4.836735
## pct.bach.deg                4.324473e+00  1        2.079537
## pct.below.pov               2.303039e+01  1        4.798999
```

```
## pct.unemp                     9.918770e+00  1        3.149408
## region                        1.985483e+09  3       35.452294
## log.per.cap.land.area:region  9.879657e+04  3        6.799187
## log.per.cap.doctors:region    2.069430e+07  3       16.569464
## pct.hs.grad:region            1.037548e+08  3       21.677109
## pct.below.pov:region          9.128360e+03  3        4.571571
## pct.unemp:region              1.689729e+04  3        5.065661
```

```
par(mfrow=c(2,2))
plot(all.subsets.01.final.with.some.region)
```



Then compare to the best BIC model that we obtained from stepwise without the `region` term.

```
# comparison
anova(all.subsets.01.final.model,all.subsets.01.final.with.some.region)
```

```
## Analysis of Variance Table
##
## Model 1: log.per.cap.income ~ log.per.cap.land.area + pop.18_34 + pop.65_plus +
##     log.per.cap.doctors + pct.hs.grad + pct.bach.deg + pct.below.pov +
##     pct.unemp
## Model 2: log.per.cap.income ~ log.per.cap.land.area + pop.18_34 + pop.65_plus +
##     log.per.cap.doctors + pct.hs.grad + pct.bach.deg + pct.below.pov +
##     pct.unemp + region + log.per.cap.land.area:region + log.per.cap.doctors:region +
##     pct.hs.grad:region + pct.below.pov:region + pct.unemp:region
##   Res.Df    RSS Df Sum of Sq      F   Pr(>F)
## 1    431 2.9031
## 2    413 2.3825 18   0.52057 5.0133 2.38e-10 ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
AIC(all.subsets.01.final.model,all.subsets.01.final.with.some.region)
```

```
##                                       df       AIC
## all.subsets.01.final.model            10 -940.5743
## all.subsets.01.final.with.some.region 28 -991.5268
```

```
BIC(all.subsets.01.final.model,all.subsets.01.final.with.some.region)
```

```
##                                       df       BIC
## all.subsets.01.final.model            10 -899.7065
## all.subsets.01.final.with.some.region 28 -877.0971
```

The anova (F test) and AIC really like the model with the region terms in it. On the other hand, BIC prefers the simpler model. Finally, we will examine the table of estimated coefficients again for the model with some region terms in it.

```
formula(all.subsets.01.final.with.some.region)
```

```
## log.per.cap.income ~ log.per.cap.land.area + pop.18_34 + pop.65_plus +
##     log.per.cap.doctors + pct.hs.grad + pct.bach.deg + pct.below.pov +
##     pct.unemp + region + log.per.cap.land.area:region + log.per.cap.doctors:region +
##     pct.hs.grad:region + pct.below.pov:region + pct.unemp:region
```

```
round(summary(all.subsets.01.final.with.some.region)$coef,2)
```

```
##                                Estimate Std. Error t value Pr(>|t|)
## (Intercept)                       10.27       0.28   36.06     0.00
## log.per.cap.land.area             -0.05       0.01   -5.86     0.00
## pop.18_34                         -0.02       0.00  -11.93     0.00
## pop.65_plus                        0.00       0.00   -1.33     0.19
## log.per.cap.doctors                0.05       0.02    3.10     0.00
## pct.hs.grad                        0.00       0.00   -1.14     0.25
## pct.bach.deg                       0.01       0.00   15.14     0.00
## pct.below.pov                     -0.02       0.00   -6.03     0.00
## pct.unemp                          0.02       0.00    3.72     0.00
## regionNE                          -0.03       0.40   -0.08     0.93
## regionS                            0.32       0.32    1.00     0.32
## regionW                            2.49       0.42    5.91     0.00
## log.per.cap.land.area:regionNE    -0.01       0.01   -0.88     0.38
## log.per.cap.land.area:regionS      0.01       0.01    1.19     0.24
## log.per.cap.land.area:regionW      0.03       0.01    2.23     0.03
## log.per.cap.doctors:regionNE       0.01       0.03    0.23     0.82
## log.per.cap.doctors:regionS        0.03       0.02    1.46     0.15
## log.per.cap.doctors:regionW        0.12       0.03    3.98     0.00
## pct.hs.grad:regionNE               0.00       0.00    0.43     0.67
## pct.hs.grad:regionS                0.00       0.00    0.04     0.96
## pct.hs.grad:regionW               -0.02       0.00   -4.59     0.00
## pct.below.pov:regionNE             0.00       0.01   -0.89     0.38
```

	df	AIC	BIC
all.subsets.01.final.model	10	-940.5743	-899.7065
step.result.01.aic	11	-942.0976	-897.1431
step.result.01.bic	10	-940.5743	-899.7065
step.result.02.aic	23	-1082.1848	-988.1890
step.result.02.bic	16	-1047.7658	-982.3774

```
## pct.below.pov:regionS              0.00       0.00    0.78      0.44
## pct.below.pov:regionW             -0.02       0.01   -3.54      0.00
## pct.unemp:regionNE                -0.01       0.01   -1.30      0.19
## pct.unemp:regionS                 -0.02       0.01   -2.64      0.01
## pct.unemp:regionW                 -0.02       0.01   -2.51      0.01
```

Appendix 4. Regression Analysis – Stepwise Regression

Two models in stepwsie regression respectively using AIC and BIC.

```
stepwise.base <- lm(log.per.cap.income ~ .,data=cdilogred.cont)

## try to duplicate all-subsets with BIC
step.result.01.bic <- stepAIC(stepwise.base,
                      scope=list(lower = ~ 1, upper = ~ .),
                      k=log(dim(cdilogred.cont)[1]),
                      trace=F)

## now try with AIC
step.result.01.aic <- stepAIC(stepwise.base,
                      scope=list(lower = ~ 1, upper = ~ .),
                      k=2,
                      trace=F)
```

Well, we will explore the models with 2-way interactions briefly.

```
step.result.02.bic <- stepAIC(stepwise.base,scope=list(lower = ~ 1, upper = ~ .^2),
                      k=log(dim(cdilogred.cont)[1]),                    ## BIC penalty.
                      trace=F)

step.result.02.aic <- stepAIC(stepwise.base,scope=list(lower = ~ 1, upper = ~ .^2),
                      k=2,                                              ## AIC penalty.
                      trace=F)

comparison <- cbind(
AIC(all.subsets.01.final.model, step.result.01.aic, step.result.01.bic,
    step.result.02.aic, step.result.02.bic),
BIC(all.subsets.01.final.model, step.result.01.aic, step.result.01.bic,
    step.result.02.aic, step.result.02.bic))
comparison <- comparison[,-3]
names(comparison) <- c("df","AIC","BIC")
comparison %>% kbl(booktabs=T) %>% kable_classic()
```

```r
# compare the R2 of two models with interactions

# step.result.02.bic
cat("\nR2 = ",summary(step.result.02.bic)$r.squared)
```

```
##
## R2 =  0.8819856
```

```r
cat("\nR2adj = ",summary(step.result.02.bic)$adj.r.squared)
```

```
##
## R2adj =  0.8780981
```

```r
# step.result.02.aic
cat("\nR2 = ",summary(step.result.02.aic)$r.squared)
```

```
##
## R2 =  0.8942832
```

```r
cat("\nR2adj = ",summary(step.result.02.aic)$adj.r.squared)
```

```
##
## R2adj =  0.8889721
```

Although both interactions models produced big jumps in AIC and BIC (much bigger than 10), the improvement in R^2 and R^2_{adj} is pretty small (less than 0.01), for all the terms that have been added to the models.

Thus, we will stick with the best model found by all-subsets and stepAIC with a BIC penalty, then my conclusions about adding interactions with `region` will also be the same.

Appendix 5. Regression Analysis – LASSO

```r
# shrinkage plot for LASSO
loc <- grep("log.per.cap.income",names(cdilogred.cont))

y <- cdilogred.cont[,loc]

X <- apply(as.matrix(cdilogred.cont[,-loc]),2,function(x) rescale(x,"full"))

Xnames <- dimnames(X)[[2]]

lasso.result <- glmnet(X,y)

plot(lasso.result,xvar="lambda",xlim=c(-9,0))

abline(h=0,lty=2)

legend('bottomright',lty=1,col=1:length(Xnames),legend=Xnames,cex=0.5)
```

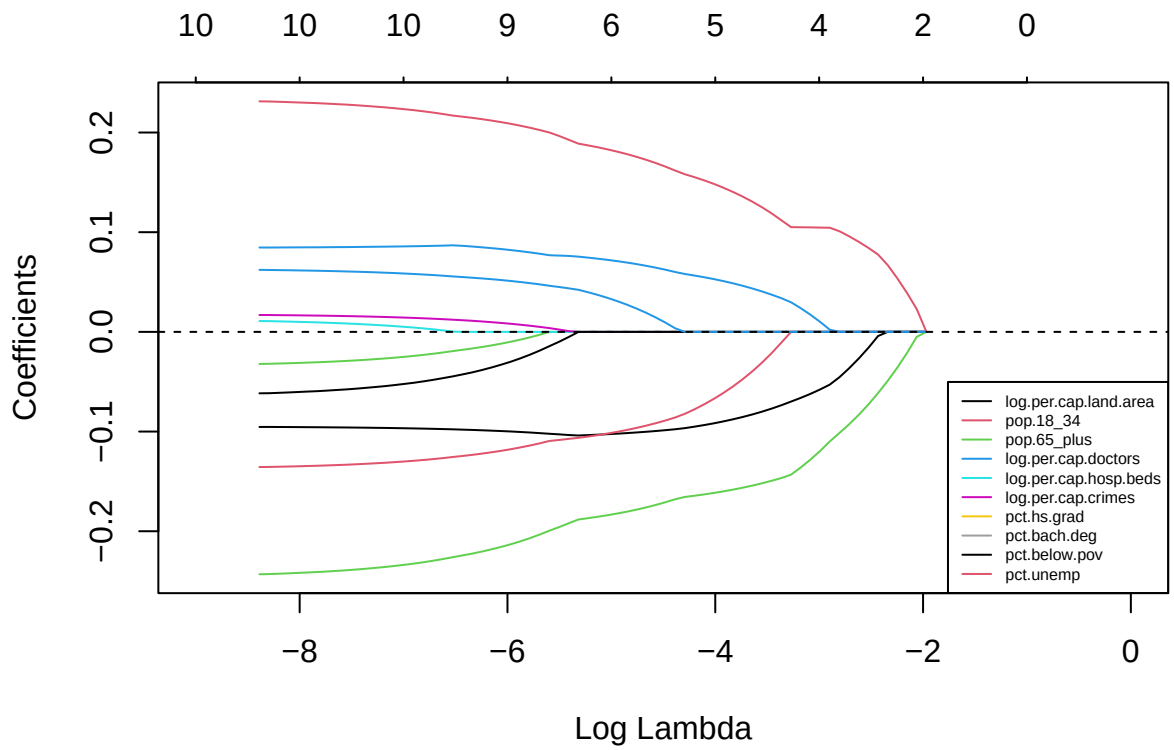
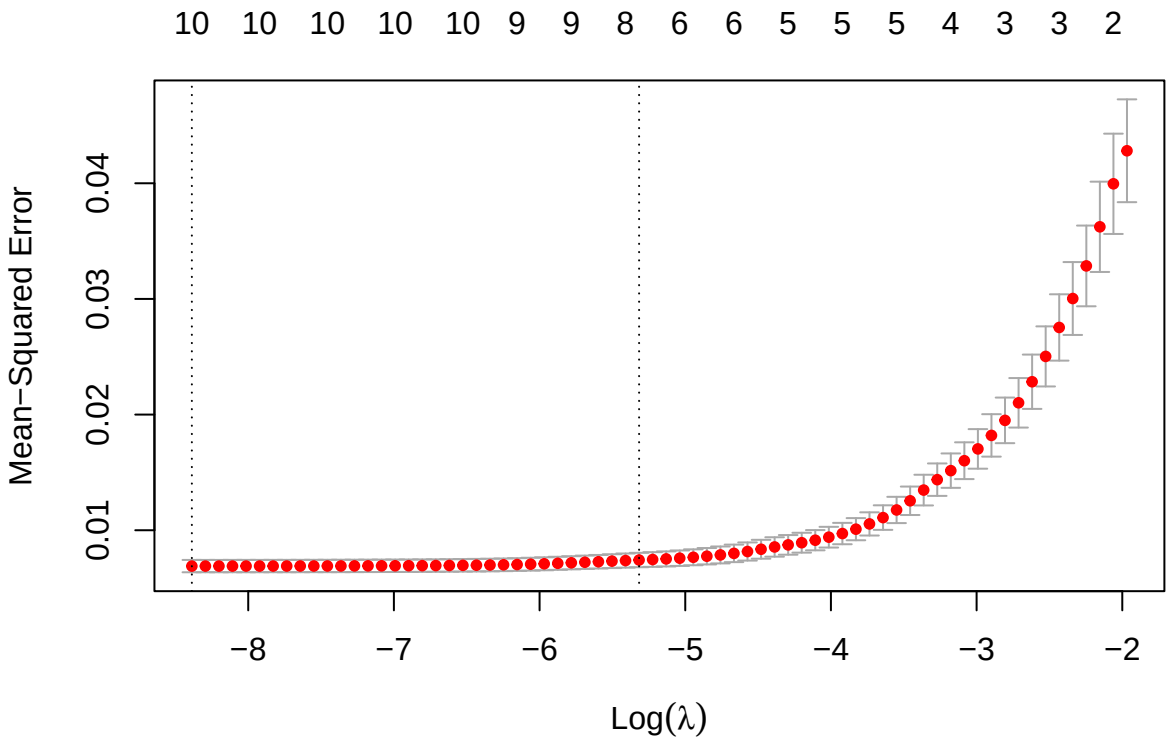


Figure 7: LASSO Variable Trace Plot.

There is not such an obvious place to cut the shrinkage plot to help determine what variables should be kept in the model.

```
# cross-valiation
cv.lasso.result <- cv.glmnet(X,y)

plot(cv.lasso.result)
```




```
c(lambda.1se=cv.lasso.result$lambda.1se,lambda.min=cv.lasso.result$lambda.min)
```

```
##   lambda.1se   lambda.min
## 0.0049081710 0.0002278171
```

```
tmp <- cbind(coef(cv.lasso.result,s=cv.lasso.result$lambda.min),
             coef(cv.lasso.result,s=cv.lasso.result$lambda.1se)
            )
dimnames(tmp)[[2]] <- c("lambda(minMSE)","lambda(minMSE+1se)")

tmp
```

```
## 11 x 2 sparse Matrix of class "dgCMatrix"
##                         lambda(minMSE) lambda(minMSE+1se)
## (Intercept)               9.80695459       9.806955e+00
## log.per.cap.land.area    -0.09536780      -1.039554e-01
## pop.18_34                -0.13561396      -1.062918e-01
## pop.65_plus              -0.03218231       .
## log.per.cap.doctors       0.08463289       7.547924e-02
## log.per.cap.hosp.beds     0.01086566       .
## log.per.cap.crimes        0.01693974       .
## pct.hs.grad              -0.06164630      -4.805525e-05
## pct.bach.deg              0.23126382       1.888050e-01
## pct.below.pov            -0.24313646      -1.881889e-01
## pct.unemp                 0.06221462       4.221509e-02
```

It's interesting to note that the model which minimizes 10-fold cross-validation error contains all 10 predictors (or sometimes 9—log.crimes can get left out—depending on the random folds). The model that is 1 SE has

2 less variable, which is `pop.65_plus` and `pct.hs.grad` than the model that we got based on the all-subsets regression.

Now let's compare these two models:

```
lasso.1se.model <- lm(log.per.cap.income ~ log.per.cap.land.area + pop.18_34
                      + log.per.cap.doctors + pct.bach.deg + pct.below.pov + pct.unemp,
                      data = cdilogred.cont)

anova(all.subsets.01.final.model,lasso.1se.model)
```

```
## Analysis of Variance Table
##
## Model 1: log.per.cap.income ~ log.per.cap.land.area + pop.18_34 + pop.65_plus +
##     log.per.cap.doctors + pct.hs.grad + pct.bach.deg + pct.below.pov +
##     pct.unemp
## Model 2: log.per.cap.income ~ log.per.cap.land.area + pop.18_34 + log.per.cap.doctors +
##     pct.bach.deg + pct.below.pov + pct.unemp
##   Res.Df    RSS Df Sum of Sq      F    Pr(>F)
## 1    431 2.9031
## 2    433 3.0592 -2   -0.1561 11.588 1.254e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
AIC(all.subsets.01.final.model,lasso.1se.model)
```

```
##                            df       AIC
## all.subsets.01.final.model 10 -940.5743
## lasso.1se.model             8 -921.5292
```

```
BIC(all.subsets.01.final.model,lasso.1se.model)
```

```
##                            df       BIC
## all.subsets.01.final.model 10 -899.7065
## lasso.1se.model             8 -888.8350
```

```
summary(lasso.1se.model)
```

```
##
## Call:
## lm(formula = log.per.cap.income ~ log.per.cap.land.area + pop.18_34 +
##     log.per.cap.doctors + pct.bach.deg + pct.below.pov + pct.unemp,
##     data = cdilogred.cont)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.37735 -0.04922 -0.00842  0.05191  0.27781
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)           10.2333158  0.0850955 120.257  < 2e-16 ***
## log.per.cap.land.area -0.0465305  0.0040070 -11.612  < 2e-16 ***
```

```
## pop.18_34             -0.0142544  0.0011372 -12.535  < 2e-16 ***
## log.per.cap.doctors    0.0769568  0.0097474   7.895 2.41e-14 ***
## pct.bach.deg           0.0134659  0.0008268  16.288  < 2e-16 ***
## pct.below.pov         -0.0216248  0.0011146 -19.402  < 2e-16 ***
## pct.unemp              0.0144028  0.0021723   6.630 1.00e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.08405 on 433 degrees of freedom
## Multiple R-squared:  0.8369, Adjusted R-squared:  0.8347
## F-statistic: 370.4 on 6 and 433 DF,  p-value: < 2.2e-16
```

```
summary(all.subsets.01.final.model)
```

```
##
## Call:
## lm(formula = log.per.cap.income ~ ., data = tmp)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.35918 -0.04920 -0.00401  0.04835  0.27154
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)            10.7858923  0.1421206  75.893  < 2e-16 ***
## log.per.cap.land.area -0.0425129  0.0040176 -10.582  < 2e-16 ***
## pop.18_34             -0.0161092  0.0013063 -12.331  < 2e-16 ***
## pop.65_plus           -0.0040409  0.0013844  -2.919   0.0037 **
## log.per.cap.doctors    0.0872129  0.0103491   8.427 5.35e-16 ***
## pct.hs.grad           -0.0045224  0.0010877  -4.158 3.88e-05 ***
## pct.bach.deg           0.0148682  0.0009586  15.510  < 2e-16 ***
## pct.below.pov         -0.0251831  0.0013295 -18.942  < 2e-16 ***
## pct.unemp              0.0129805  0.0021976   5.907 7.09e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.08207 on 431 degrees of freedom
## Multiple R-squared:  0.8453, Adjusted R-squared:  0.8424
## F-statistic: 294.3 on 8 and 431 DF,  p-value: < 2.2e-16
```

Though F-test prefers the model that is 1 SE based on LASSO, both AIC and BIC prefers the original model based on the all-subsets regression. All the coeffiecients for variables in both 2 model are statistically significant. So for better interpretation and the integrality of the model, we will settle on the very first model we got based on the all-subsets regression.